

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E

(ii) TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE

(iii) NUMBER OF SEQUENCES: 183

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
(B) STREET: 600 South Avenue West
(C) CITY: Westfield
(D) STATE: New Jersey
(E) COUNTRY: U.S.A.
(F) ZIP: 07090

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Microsoft Word, Version 6.0c

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/509,359
(B) FILING DATE: 31-JUL-95
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Palisi, Thomas M.
(B) REGISTRATION NUMBER: 36629

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (908) 654-5000
(B) TELEFAX: (908) 654-7866

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGGCGC AGCGGGGCAG CGGGGNAAGC GTATACCTAA	120
TCTGGGAGCC TGCAAGTGAC AACAGCCTTT GCGGTCTTA GACAGCTTGG CCTGGAGGAG	180
AACACATGAA AGAAAGAACCC TCAAGAGGCT TTGTTTCTG TGAAACAGTA TTTCTATACA	240
GTTGCTCCAA TGACAGAGTT ACCTGCACCG TTGTCCTACT TCCAGAATGC ACAGATGTCT	300

GAGGACAACC	ACCTGAGCAA	TACTGTACGT	AGCCAGAATG	ACAATAGAGA	ACGGCAGGAG	360
CACAACGACA	GACGGAGCCT	TGGCCACCCCT	GAGCCATTAT	CTAATGGACG	ACCCCAGGGT	420
AACTCCCAGC	AGGTGGTGGA	GCAAGATGAG	GAAGAAGATG	AGGAGCTGAC	ATTGAAATAT	480
GGCGCCAAGC	ATGTGATCAT	GCTCTTGTC	CCTGTGACTC	TCTGCATGGT	GGTGGTCGTG	540
GCTACCATTA	AGTCAGTCAG	CTTTTATACC	CGGAAGGATG	GGCAGCTAAT	CTATACCCCA	600
TTCACAGAAG	ATACCGAGAC	TGTGGGCCAG	AGAGCCCTGC	ACTCAATTCT	GAATGCTGCC	660
ATCATGATCA	GTGTCATTGT	TGTCATGACT	ATCCTCCTGG	TGGTTCTGTA	TAAATACAGG	720
TGCTATAAGG	TCATCCATGC	CTGGCTTATT	ATATCATCTC	TATTGTTGCT	GTTCTTTTT	780
TCATTCAATT	ACTTGGGGGA	AGTGTAAAC	ACCTATAACG	TTGCTGTGGA	CTACATTACT	840
GTTGCACTCC	TGATCTGGAA	TTTGGGTGTG	GTGGGAATGA	TTTCCATTCA	CTGGAAAGGT	900
CCACTTCGAC	TCCAGCAGGC	ATATCTCATT	ATGATTAGTG	CCCTCATGGC	CCTGGTGTGTT	960
ATCAAGTACC	TCCCTGAATG	GACTGCGTGG	CTCATCTTGG	CTGTGATTTC	AGTATATGAT	1020
TTAGTGGCTG	TTTGTGTCC	GAAAGGTCCA	CTTCGTATGC	TGGTTGAAAC	AGCTCAGGAG	1080
AGAAATGAAA	CGCTTTTCC	AGCTCTCATT	TACTCCTCAA	CAATGGTGTG	GTTGGTGAAT	1140
ATGGCAGAAG	GAGACCCGGA	AGCTCAAAGG	AGAGTATCCA	AAAATTCAA	GTATAATGCA	1200
GAAAGCACAG	AAAGGGAGTC	ACAAGACACT	GTTGCAGAGA	ATGATGATGG	CGGGTTCACT	1260
GAGGAATGGG	AAGCCCAGAG	GGACAGTCAT	CTAGGGCCTC	ATCGCTCTAC	ACCTGAGTCA	1320
CGAGCTGCTG	TCCAGGAAC	TTCCAGCAGT	ATCCTCGCTG	GTGAAGACCC	AGAGGAAAGG	1380
GGAGTAAAC	TTGGATTGGG	AGATTCATT	TTCTACAGTG	TTCTGGTTGG	TAAAGCCTCA	1440
GCAACAGCCA	GTGGAGACTG	GAACACAACC	ATAGCCTGTT	TCGTAGCCAT	ATTAATTGGT	1500
TTGTGCCTTA	CATTATTACT	CCTTGCCATT	TTCAAGAAAG	CATTGCCAGC	TCTTCCAATC	1560
TCCATCACCT	TTGGGCTTGT	TTTCTACTTT	GCCACAGATT	ATCTTGTACA	GCCTTTATG	1620
GACCAATTAG	CATTCCATCA	ATTTTATATC	TAGCATATT	GCGGTTAGAA	TCCCATGGAT	1680
GTTTCTTCTT	TGACTATAAC	CAAATCTGGG	GAGGACAAAG	GTGATTTCC	TGTGTCCACA	1740
TCTAACAAAG	TCAAGATTCC	CGGCTGGACT	TTTGCAGCTT	CCTTCCAAGT	CTTCCTGACC	1800
ACCTTGCACT	ATTGGACTTT	GGAAGGAGGT	GCCTATAGAA	AACGATTTG	AACATACTTC	1860
ATCGCAGTGG	ACTGTGTCC	CGGTGCAGAA	ACTACCAGAT	TTGAGGGACG	AGGTCAAGGA	1920
GATATGATAG	GCCCCGGAAGT	TGCTGTGCC	CATCAGCAGC	TTGACCGCTG	GTCACAGGAC	1980
GATTTCACTG	ACACTGCGAA	CTCTCAGGAC	TACCGGTTAC	CAAGAGGTTA	GGTGAAGTGG	2040
TTTAAACCAA	ACGGAACACT	TCATCTAAA	CTACACGTTG	AAAATCAACC	CAATAATTCT	2100
GTATTAAC	TGAAAC	TTTCAGGAG	GTACTGTGAG	GAAGAGCAGG	CACCAGCAGC	2160
AGAATGGGGGA	ATGGAGAGGT	GGGCAGGGGT	TCCAGCTTCC	CTTTGATTTT	TTGCTGCAGA	2220

CTCATCCTT TTAAATGAGA CTTGTTTCC CCTCTCTTG AGTCAAGTCA AATATGTAGA	2280
TGCCTTGGC AATTCTTCTT CTCAAGCACT GACACTCATT ACCGTCTGTG ATTGCCATT	2340
CTTCCAAGG CCAGTCTGAA CCTGAGGTTG CTTTATCCTA AAAGTTTAA CCTCAGGTT	2400
CAAATTCAAGT AAATTTGGA AACAGTACAG CTATTTCTCA TCAATTCTCT ATCATGTTGA	2460
AGTCAAATT GGATTTCCA CCAAATTCTG AATTGTAGA CATACTGTA CGCTCACTG	2520
CCCCAGATGC CTCCTCTGTC CTCATTCTTC TCTCCCACAC AAGCAGTCTT TTTCTACAGC	2580
CAGTAAGGCA GCTCTGTCGT GGTAGCAGAT GGTCCCACCTT ATTCTAGGGT CTTACTCTT	2640
GTATGATGAA AAGAATGTGT TATGAATCGG TGCTGTCAGC CCTGCTGTCA GACCTTCTTC	2700
CACAGCAAAT GAGATGTATG CCCAAAGCGG TAGAATTAAA GAAGAGTAAA ATGGCTGTTG	2760
AAGCAAAAAA AAAAAAAA AAAAAAAA A	2791

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met	
1 5 10 15	
Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn	
20 25 30	
Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu	
35 40 45	
Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu	
50 55 60	
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys	
65 70 75 80	
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val	
85 90 95	
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln	
100 105 110	
Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg	
115 120 125	
Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val	
130 135 140	
Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys	
145 150 155 160	

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
 165 170 175
 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
 180 185 190
 Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Leu Gly Val Val
 195 200 205
 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
 210 215 220
 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
 225 230 235 240
 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
 245 250 255
 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
 260 265 270
 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
 275 280 285
 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
 290 295 300
 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
 305 310 315 320
 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
 325 330 335
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
 340 345 350
 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
 355 360 365
 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
 370 375 380
 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
 385 390 395 400
 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
 405 410 415
 Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
 420 425 430
 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
 435 440 445
 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
 450 455 460
 Phe Tyr Ile
 465

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1929 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACCANACANC	GGCAGCTGAG	GCGGAAACCT	AGGCTGCGAG	CCGGCCGCC	GGGCGGGAG	60
AGAGAAGGAA	CCAACACAAG	ACAGCAGCCC	TTCGAGGTCT	TTAGGCAGCT	TGGAGGAGAA	120
CACATGAGAG	AAAGAATCCC	AAGAGGTTT	GTTTCTTG	AGAAGGTATT	TCTGTCCAGC	180
TGCTCCAATG	ACAGAGATAC	CTGCACCTT	GTCCTACTTC	CAGAATGCC	AGATGTCTGA	240
GGACAGCCAC	TCCAGCAGCG	CCATCCGGAG	CCAGAATGAC	AGCCAAGAAC	GGCAGCAGCA	300
GCATGACAGG	CAGAGACTTG	ACAACCCTGA	GCCAATATCT	AATGGCGGC	CCCAGAGTAA	360
CTCAAGACAG	GTGGTGGAAC	AAGATGAGGA	GGAAAGACGAA	GAGCTGACAT	TGAAATATGG	420
AGCCAAGCAT	GTCATCATGC	TCTTGTC	CGTGACCC	TGCATGGTC	TCGTCGTGGC	480
CACCATCAAA	TCAGTCAGCT	TCTATACCCG	GAAGGACGGT	CAGCTAATCT	ACACCCATT	540
CACAGAAGAC	ACTGAGACTG	TAGGCCAAAG	AGCCCTGCAC	TCGATCCTGA	ATGCGGCCAT	600
CATGATCAGT	GTCATTGTCA	TTATGACCAT	CCTCCTGGTG	GTCCTGTATA	AATACAGGTG	660
CTACAAGGTC	ATCCACGCCT	GGCTTATTAT	TTCATCTCTG	TTGTTGCTGT	TCTTTTTTC	720
GTTCAATTAC	TTAGGGGAAG	TATTAAGAC	CTACAATGTC	KCCGTGGACT	ACGTTACAGT	780
AGCACTCCTA	ATCTGGAATT	GGGGTGTGGT	CGGGATGATT	GCCATCCACT	GGAAAGGCC	840
CCTTCGACTG	CAGCAGGC	GT ATCTCATTAT	GATCAGTGCC	CTCATGGCC	TGGTATTAT	900
CAAGTACCTC	CCCGAATGGA	CCGCATGGCT	CATCTGGCT	GTGATTCAG	TATATGATT	960
GGTGGCTGTT	TTATGTCCA	AAGGCCACT	TCGTATGCTG	GTTGAAACAG	CTCAGGAAAG	1020
AAATGAGACT	CTCTTCCAG	CTCTTATCTA	TTCCCTAAC	ATGGTGTGGT	TGGTGAATAT	1080
GGCTGAAGGA	GACCCAGAAG	CCCAAAGGAG	GGTACCCAAG	AACCCCAAGT	ATAACACACA	1140
AAGAGCGGAG	AGAGAGACAC	AGGACAGTGG	TTCTGGAAC	GATGATGGTG	GCTTCAGTGA	1200
GGAGTGGGAG	GCCCCAAAGAG	ACAGTCACCT	GGGGCCTCAT	CGCTCCACTC	CCGAGTCAAG	1260
AGCTGCTGTC	CAGGAAC	CTGGGAGCAT	TCTAACGAGT	GAAGACCCGG	AGGAAAGAGG	1320
AGTAAAAC	TTT	CTACAGTGT	CTGGTTGGTA	AGGCCTCAGC	1380	
AACCGCCAGT	GGAGACTGGA	ACACAACC	AGCCTGCTT	GTAGCCATAC	TGATCGGC	1440
GTGCCTTANA	TTACTCCTGC	TCGCCATT	CAAGAAAGGG	TNGCCAGCCC	NCCCCATCTC	1500

CATCACCTTC GGGTCGTGT TCTNCTTCGC CACGGATTAC CTTGTGCAGC CCTTCATGGA	1560
CCAACTTGCA TTCCATCAGT TTTATATCTA GCCTTCAGC AGTTAGAACCA TGGATGTTTC	1620
TTCTTGATT ATCAAAACA CAAAAACAGA GAGCAAGCCC GAGGAGGAGA CTGGTGACTT	1680
TCCTGTGTCC TCAGCTAACCA AAGGCAGGAC TCCAGCTGGA CTTCTGCAGC TTCCTTCGA	1740
GTCTCCCTAG CCACCCGCAC TACTGGACTG TGGAGGAAG CGTCTACAGA GGAACGGTTT	1800
CCAACATCCA TCGCTGCAGC AGACGGTGTG CTCAGTGAC TTGAGAGACA AGGACAAGGA	1860
AATGTGCTGG GCCAAGGAGC TGCCGTGCTC TGCTAGCTTT GGMCCGTGGG CATGGAGATT	1920
TACCCGCAC	1929

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Glu Ile Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met	
1 5 10 15	
Ser Glu Asp Ser His Ser Ser Ala Ile Arg Ser Gln Asn Asp Ser	
20 25 30	
Gln Glu Arg Gln Gln His Asp Arg Gln Arg Leu Asp Asn Pro Glu	
35 40 45	
Pro Ile Ser Asn Gly Arg Pro Gln Ser Asn Ser Arg Gln Val Val Glu	
50 55 60	
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys	
65 70 75 80	
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val	
85 90 95	
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln	
100 105 110	
Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg	
115 120 125	
Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val	
130 135 140	
Ile Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys	
145 150 155 160	
Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe	
165 170 175	
Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Xaa	

180	185	190	
Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Trp Gly Val Val			
195	200	205	
Gly Met Ile Ala Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala			
210	215	220	
Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr			
225	230	235	240
Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr			
245	250	255	
Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val			
260	265	270	
Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr			
275	280	285	
Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu			
290	295	300	
Ala Gln Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala			
305	310	315	320
Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Gly Phe			
325	330	335	
Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg			
340	345	350	
Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile			
355	360	365	
Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly			
370	375	380	
Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala			
385	390	395	400
Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Xaa Val Ala Ile Leu Ile			
405	410	415	
Gly Leu Cys Leu Xaa Leu Leu Leu Ala Ile Tyr Lys Lys Gly Xaa			
420	425	430	
Pro Ala Xaa Pro Ile Ser Ile Thr Phe Gly Phe Val Phe Xaa Phe Ala			
435	440	445	
Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln			
450	455	460	
Phe Tyr Ile			
465			

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3087 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTGGCGA CGAGGGAAAT GCTGTTGCT CGAAGACGTC TCAGGGCGCA GGTGCCTTGG	60
GCCGGGATTA GTAGCCGTCT GAACTGGAGT GGAGTAGGAG AAAGAGGAAG CGTCTTGGC	120
TGGGTCTGCT TGAGCAACTG GTGAAACTCC GCGCCTCACG CCCCGGGTGT GTCCTTGTCC	180
AGGGGCGACG AGCATTCTGG GCGAAGTCCG CACSCCTCTT GTTCGAGGCG GAAGACGGGG	240
TCTGATSC TTCTCCCTGGT CGGGMCTGTC TCGAGGCATG CATGTCCAGT GACTCTTGTG	300
TTTGCTGCTG CTTCCCTCTC AGATTCTTCT CACCGTTGTG GTCAGCTCTG CTTTAGGCAN	360
TATTAATCCA TAGTGGAGGC TGGGATGGGT GAGAGAATTG AGGTGACTTT TCCATAATTC	420
AGACCTAATC TGGGAGCCTG CAAGTGACAA CAGCCTTGC GGTCCCTAGA CAGCTTGGCC	480
TGGAGGAGAA CACATGAAAG AAAGAACCTC AAGAGGCTTT GTTTTCTGTG AAACAGTATT	540
TCTATACAGT TGCTCCAATG ACAGAGTTAC CTGCACCGTT GTCCTACTTC CAGAATGCAC	600
AGATGTCTGA GGACAACCAC CTGAGCAATA CTAATGACAA TAGAGAACGG CAGGAGCACA	660
ACGACAGACG GAGCCTTGGC CACCCTGAGC CATTATCTAA TGGACGACCC CAGGGTAACT	720
CCCGGCAGGT GGTGGAGCAA GATGAGGAAG AAGATGAGGA GCTGACATTG AAATATGGCG	780
CCAAGCATGT GATCATGCTC TTTGTCCCTG TGACTCTCTG CATGGTGGTG GTCGTGGCTA	840
CCATTAAGTC AGTCAGCTTT TATAACCGGA AGGATGGCA GCTAATCTAT ACCCCATTCA	900
CAGAAGATAC CGAGACTGTG GGCCAGAGAG CCCTGCACTC AATTCTGAAT GCTGCCATCA	960
TGATCAGTGT CATTGTTGTC ATGACTATCC TCCTGGTGGT TCTGTATAAA TACAGGTGCT	1020
ATAAGGTCA CCATGCCTGG CTTATTATAT CATCTCTATT GTTGCTGTTC TTTTTTCAT	1080
TCATTTACTT GGGGGAAGTG TTTAAAACCT ATAACGTTGC TGTGGACTAC ATTACTGTTG	1140
CACTCCTGAT CTGGAATTG GGTGTGGTGG GAATGATTTC CATTCACTGG AAAGGTCCAC	1200
TTCGACTCCA GCAGGCATAT CTCATTATGA TTAGTGCCCT CATGGCCCTG GTGTTTATCA	1260
AGTACCTCCC TGAATGGACT GCGTGGCTCA TCTTGGCTGT GATTCAGTA TATGATTTAG	1320
TGGCTGTTT GTGTCCGAAA GGTCCACTTC GTATGCTGGT TGAAACAGCT CAGGAGAGAA	1380
ATGAAACGCT TTTTCCAGCT CTCATTTACT CCTCAACAAT GGTGTGGTTG GTGAATATGG	1440
CAGAAGGAGA CCCGGAAGCT CAAAGGAGAG TATCCAAAAA TTCCAAGTAT AATGCAGAAA	1500
GCACAGAAAG GGAGTCACAA GACACTGTTG CAGAGAATGA TGATGGCGGG TTCAGTGAGG	1560
AATGGGAAGC CCAGAGGGAC AGTCATCTAG GGCCTCATCG CTCTACACCT GAGTCACGAG	1620
CTGCTGTCCA GGAACCTTCC AGCAGTATCC TCGCTGGTGA AGACCCAGAG GAAAGGGGAG	1680
TAAAACCTGG ATTGGGAGAT TTCATTTCT ACAGTGTCT GGTTGGTAAA GCCTCAGCAA	1740
CAGCCAGTGG AGACTGGAAC ACAACCATAG CCTGTTCGT AGCCATATTA ATTGGTTGT	1800

GCCTTACATT ATTACTCCTT GCCATTTCA AGAAAGCATT GCCAGCTCTT CCAATCTCCA	1860
TCACCTTGG GCTTGTTC TACTTGCCTA CAGATTATCT TGTACAGCCT TTTATGGACC	1920
AATTAGCATT CCATCAATT TATATCTAGC ATATTCGCGG TTAGAATCCC ATGGATGTTT	1980
CTTCTTGAC TATAACCAAA TCTGGGGAGG ACAAAAGGTGA TTTTCCGTG TCCACATCTA	2040
ACAAAGTCAA GATTCCCGGC TGGACTTTG CAGCTCCTT CCAAGTCTTC CTGACCACCT	2100
TGCACTATTG GACTTGGAA GGAGGTGCCT ATAGAAAACG ATTTGAACA TACTTCATCG	2160
CAGTGGACTG TGTCCCTCGGT GCAGAAACTA CCAGATTGA GGGACGAGGT CAAGGAGATA	2220
TGATAGGCC GGAAGTTGCT GTGCCCATC AGCAGCTTGA CGCGTGGTCA CAGGACGATT	2280
TCACTGACAC TGCGAACTCT CAGGACTACC GGTTACCAAG AGGTTAGGTG AAGTGGTTA	2340
AACCAAACGG AACTCTTCAT CTTAAACTAC ACGTTGAAAA TCAACCCAAT AATTCTGTAT	2400
TAACTGAATT CTGAACTTTT CAGGAGGTAC TGTGAGGAAG AGCAGGCACC AGCAGCAGAA	2460
TGGGAATGG AGAGGTGGC AGGGGTTCCA GCTTCCCTT GATTTTTGC TGCAGACTCA	2520
TCCTTTTAA ATGAGACTTG TTTTCCCTC TCTTGAGTC AAGTCAAATA TGTAGATGCC	2580
TTGGCAATT CTTCTCTCA AGCACTGACA CTCATTACCG TCTGTGATTG CCATTTCTC	2640
CCAAGGCCAG TCTGAACCTG AGGTTGCTT ATCCTAAAAG TTTAACCTC AGGTTCCAAA	2700
TTCAGTAAAT TTTGGAAACA GTACAGCTAT TTCTCATCAA TTCTCTATCA TGTGAAGTC	2760
AAATTTGGAT TTTCCACCAA ATTCTGAATT TGTAGACATA CTTGTACGCT CACTTGCCCC	2820
AGATGCCTCC TCTGCTCTCA TTCTCTCTC CCACACAAAGC AGTCTTTTC TACAGCCAGT	2880
AAGGCAGCTC TGTGTTGGTA GCAGATGGTC CCACTTATTC TAGGGTCTTA CTCTTGAT	2940
GATGAAAAGA ATGTGTTATG AATCGGTGCT GTCAGCCCTG CTGTCAGACC TTCTCCACA	3000
GCAAATGAGA TGTATGCCA AAGCGGTAGA ATAAAGAAG AGTAAAATGG CTGTTGAAGC	3060
AAAAAAAAAA AAAAAAAAAA AAAAAAA	3087

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTNTCCNAA CCAACTTAGG AGNTTGGACC TGGGRAAGAC CNACNTGATC TCCGGGAGGN	60
AAAGACTNCA GTTGAGCCGT GATTGCACCC ACTTTACTCC AAGCCTGGC AACCAAAATG	120
AGACACTGGC TCCAAACACA AAAACAAAAA CAAAAAAAGA GTAAATTAAT TTANAGGGAA	180

GNATTAAATA AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGANA	240
TTAATATCTA ATGTTGGGA GCCATCACAT TATTCTAAAT AATGTTTGG TGAAATTAT	300
TGTACATCTT TTAAAATCTG TGTAATTGGT TTTCAGGGAA GTGTTAAAA CCTATAACGT	360
TGCTGTGGAC TACATTACTG TTNCACTCCT GATCTGGAAT TTTGGTGTGG TGGGAATGAT	420
TTCCATTACAC TGGAAAGGTC CACTTCGACT CCAGCAGGCA TATCTCATTA TGATTAGTGC	480
CCTCATGNCC CTGKTGTTA TCAAGTACCT CCCTGAATGG ACTGNGTGGC TCATCTTGGC	540
TGTGATTCA GTATATGGTA AAACCCAAGA CTGATAATTG GTTGTACACA GGAATGCC	600
ACTGGAGTGT TTTCTTCCT CATCTCTTA TCTTGATTAA GAGAAAATGG TAACGTGTAC	660
ATCCCATAAC TCTTCAGTAA ATCATTAATT AGCTATAGTA ACTTTTCAT TTGAAGATT	720
CGGCTGGGCA TGGTAGCTCA TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCGGGCAG	780
ATCACCTAAG CCCAGAGTTC AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA	840
GAAAATACAA AAATTAGCCG GGCATGGTGG TGCACACCTG TAGTTCCAGC TACTTAGGAG	900
GCTGAGGTGG GAGGATCGAT TGATCCCAGG AGGTCAAGNC TGCAG	945

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTTGCAAAGT CATGGATTCC TTTAGGTAGC TACATTATCA ACCTTTTGA GAATAAAATG	60
AATTGAGAGT GTTACAGTCT AATTCTATAT CACATGTAAC TTTTATTTGG ATATATCAGT	120
AATAGTGCTT TTTTTTTTT TTTTTTTTT TTTTTTTTT TTTGGGGANA GAGTCTCGCT	180
CTGTCGCCAG GTTGGAGTGC AATGGTGCAG TCTGGCTCA CTGAAAGCTC CACCNCCCCG	240
GTTCAAGTGA TTCTCCTGCC TCAGCCNCCC AAGTAGNTGG GACTACAGGG GTGCGCCACC	300
ACGCCTGGGA TAATTTGGG NTTTTAGTA GAGATGGCGT TTCACCANCT TGGNGCAGGC	360
TGGTCTTGGGA ACTCCTGANA TCATGATCTG CCTGCCTTAG CCTCCCCAAA GTGCTGGGAT	420
TNCAGGGGTG AGCCACTGTT CCTGGGCCTC	450

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTCATCATG CTTCACGGGG GAGGCTGTGC GGGAAAGAATG CTCCCACACA GNATAAAAGAA	60
TGCTCCCGCA CAGGATAGAG AATGCCCG CACAGCATAG AGAAGCCCCC GCACAGCATA	120
GAGAATGCC CCNCACAGCA TAGAGAAGCC CCCGCACAGC ATAGAGAATG CTCTTCACCT	180
CTGGGTTTT AACCAGCCAA ACTAAAATCA CAGAGGSCMA CACATCATT AAGATAGAAA	240
TTTCTGTATC TTTTAATTY TTTCMAGTA GTTTTACTTA TTTTCAGATT CTATTTCTTT	300
ACTAGAATTA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACMAACMMAA	360
GCTAGGTTTT TTTCATAGST CTTCTTCAG ATTGAATGAA CGTCTGTTCT AAAATTTAAC	420
CCCCCAGGGA AATATTCACT TAACATATGTT AAAAACCCAG ACTTGTGATT GAGTTTGCC	480
TGAAAATGCT TTCATAATTA TGTGTGAATG TGTGTC	516

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1726 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGATCCCTCC CCTTTTACA CCATACAAGG TAACTTCCGG ACGTTGCCAT GGCATCTGTA	60
AACTGTCATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA	120
TAGTGAGCAG TGAGGATAAC CAGAGGTAC TCTCCTCACC ATCTTGGTTT TGGTGGGTTT	180
TGGCCAGCTT CTTTATTGCA ACCAGTTTA TCAGCAAGAT CTTTATGAGC TGTATCTTGT	240
GCTGACTTCC TATCTCATCC CGNAACTAAG AGTACCTAAC CTCCTGCAA TTGMAGNCCA	300
GNAGGTCTTG GNCTTATTTN ACCCAGCCCC TATTCAARAT AGAGTNGYTC TTGGNCCAAA	360
CGCCYCTGAC ACAAGGATT TAAAGTCTTA TTAATTAAGG TAAGATAGKT CCTTGSATAT	420
GTGGTCTGAA ATCACAGAAA GCTGAATTG GAAAAAGGTG CTTGGASCTG CAGCCAGTAA	480
ACAAGTTTC ATGCAGGTGT CAGTATTAA GGTACATCTC AAAGGATAAG TACAATTGTG	540
TATGTTGGGA TGAACAGAGA GAATGGAGCA ANCCAAGACC CAGGTAAAAG AGAGGACCTG	600
AATGCCTTCA GTGAACAATG ATAGATAATC TAGACTTTA AACTGCATAC TTCTGTACA	660
TTGTTTTTC TTGCTTCAGG TTTTAGAAC TCATAGTGAC GGGTCTGTTG TTAATCCAG	720

GTCTAACCGT TACCTTGATT CTGCTGAGAA TCTGATTAC TGAAAATGTT TTTCTTGTGC	780
TTATAGAATG ACAATAGAGA ACGGCAGGAG CACAACGACA GACGGAGCCT TGGCCACCC	840
GANCCATTAT CTAATGGACG ACCCAGGGTA ACTCCCGCA GGTGGTGGAN CAAGATGAGG	900
AAGAAGATGA GGAGCTGACA TTGAAATATG NCGSCAAGCA TGTGATCATG CTCTTTGKCC	960
CTGTGACTCT CTGCATGGTG GTGGTCGTGG NTACCATTA GTCAGTCAGC TTTTATACCC	1020
GGAAGGATGG GCAGCTGTAC GTATGAGTTT KGTGTTATTA TTCTCAAASC CAGTGTGGCT	1080
TTTCTTTACA GCATGTCATC ATCACCTTGA AGGCCTCTNC ATTGAAGGGG CATGACTTAG	1140
CTGGAGAGCC CATCCTCTGT GATGGTCAGG AGCAGTTGAG AGANCGAGGG GTTATTACTT	1200
CATGTTTAA GTGGAGAAAA GGAACACTGC AGAAGTATGT TTCCTGTATG GTATTACTGG	1260
ATAGGGCTGA AGTTATGCTG AATTGAACAC ATAAATTCTT TTCCACCTCA GGGNCATTGG	1320
GCGCCCATTG NTCTTCTGCC TAGAATATTC TTTCCATTNC TNACTKGNN GGATTAAATT	1380
CCTGTATCC CCCTCCTCTT GGTGTTATAT ATAAAGTNTT GGTGCCGCAA AAGAAGTAGC	1440
ACTCGAATAT AAAATTTCC TTTTAATTCT CAGCAAGGNA AGTTACTTCT ATATAGAAGG	1500
GTGCACCCNT ACAGATGGAA CAATGGCAAG CGCACATTG GGACAAGGGG GGGGAAAGGG	1560
TTCTTATCCC TGACACACGT GGTCCNGCT GNTGTGTNCT NCCCCACTG ANTAGGGTTA	1620
GACTGGACAG GCTTAAACTA ATTCCAATTG GNTAATTAA AGAGAATNAT GGGGTGAATG	1680
CTTGGGAGG AGTCAAGGAA GAGNAGGTAG NAGGTAACCTT GAATGA	1726

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CNCGTATAAA AGACCAACAT TGCCANCNAC AACCAACAGGC AAGATCTTCT CCTACCTTCC	60
CCCNNGGTGT AATACCAAGT ATTNCNAAT TTGTGATAAA CTTCATTGG AAAGTGACCA	120
CCCTCCTTGG TTAATACATT GTCTGTGCCT GCTTCACAC TACAGTAGCA CAGTTGAGTG	180
TTTGCCCTGG AGACCATATG ACCCATAGAG CTTAAATAT TCAGTCTGGC TTTTACAGA	240
GATGTTTCTG ACTTTGTTAA TAGAAAATCA ACCCAACTGG TTTAAATAAT GCACATACTT	300
TCTCTCTCAT AGAGTAGTGC AGAGGTAGNC AGTCCAGATT AGTASGGTGG CTTCACGTT	360
ATCCAAGGAC TCAATCTCCT TCTTTCTCT TTAGCTTCTA ACCTCTAGCT TACTTCAGGG	420
TCCAGGCTGG AGCCCTASCC TTCATTCTG ACAGTAGGAA GGAGTAGGGG AGAAAAGAAC	480

ATAGGACATG TCAGCAGAAT TCTCTCCTTA GAAGTTCCAT ACACAACACA TCTCCCTAGA	540
AGTCATTGCC CTTACTTGTT CTCATAGCCA TCCTAAATAT AAGGGAGTCA GAAGTAAAGT	600
CTKKNTGGCT GGGAAATATTG GCACCTGGAA TAAAAATGTT TTTCTGTGAA TGAGAAACAA	660
GGGAAAGATG GATATGTGAC ATTATCTAA GACAACCTCA GTTGCAATT A CTCTGCAGAT	720
GAGAGGCAC T AATTATAAGC CATATTACCT TTCTCTGAC AACCACTTGT CAGCCCNCGT	780
GGTTTCTGTG GCAGAAATCTG GTTCYATAMC AAGTTCC TAA TAANCTGTAS CCNAAAAAAT	840
TTGATGAGGT ATTATAATTA TTTCAATATA AAGCACCCAC TAGATGGAGC CAGTGTCTGC	900
TTCACATGTT AAGTCCTTCT TTCCATATGT TAGACATTCTT CTTTGAAGCA ATTTTAGAGT	960
GTAGCTGTT TTCTCAGGTT AAAAATTCTT AGCTAGGATT GGTGAGTTGG GGAAAAGTGA	1020
CTTATAAGAT NCGAATTGAA TTAAGAAAAA GAAAATTCTG TGTTGGAGGT GGTAAATGTGG	1080
KTGGTGATCT YCATTAACAC TGANCTAGGG CTTKGKGTT TGKTTTATTG TAGAATCTAT	1140
ACCCCATTCA NAGAAGATAC CGAGACTGTG GGCCAGAGAG CCCTGCACTC AATTCTGAAT	1200
GCTGCCATCA TGATCAGNGT CATTGTWGTC ATGACTANN CTCCTGGTGGT TCWGTATAAA	1260
TACAGGTGCT ATAAGGTGAG CATGAGACAC AGATCTTGN TTTCCACCCCT GTTCTTCTTA	1320
TGGTTGGGTA TTCTTGTAC AGTAACCTAA CTGATCTAGG AAAGAAAAAA TGTTTTGTCT	1380
TCTAGAGATA AGTTAATTT TAGTTTCTT CCTCCTCACT GTGGAACATT CAAAAAATAC	1440
AAAAAGGAAG CCAGGTGCAT GTGTAATGCC AGGCTCAGAG GCTGAGGCAG GAGGATCGCT	1500
TGGGCCAGG AGTCACAAG CAGCTTGGGC AACGTAGCAA GACCCTGCCT CTATTAAAGA	1560
AAACAAAAAA CAAATATTGG AAGTATTTA TATGCATGGA ATCTATATGT CATGAAAAAA	1620
TTAGTGTAAA ATATATATAT TATGATTAGN TATCAAGATT TAGTGATAAT TTATGTTATT	1680
TTGGGATTT AATGCCCTTT TAGGCCATTG TCTCAAMAAA TAAAAGCAGA AAACAAAAAA	1740
AGTTGTAAC T GAAAAATAAA CATTCCATA TAATAGCACA ATCTAAGTGG GTTTTGNTT	1800
GT TTTGTTGN TTGTTGAAGC AGGGCCTTGC CCTNYCACCC AGGNTGGAGT GAA GTGCAGT	1860
GGCACGATT TGGCTCACTG CAG	1883

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAGGAGTGG A CTAGGTAAAT GNAAGNTGTT TTAAAGAGAG ATGNGGN CNG GGACATAGT G

60

GTACACANCT	GTAATGCTCA	NCACTKATGG	GGAGTACTGA	AGGNGGNSGG	ATCACTTGNG	120
GGTCNGGAAT	NTGAGANCAG	CCTGGGCAAN	ATGGCGAAAC	CCTGTCTCTA	CTAAAAATAG	180
CCANAAWNWA	GCCTAGCGTG	GTGGCGCRCA	CGCGTGGTTC	CACCTACTCA	GGAGGCNTAA	240
GCACGAGNAN	TNCTTGAACC	CAGGAGGCAG	AGGNTGTGGT	GARCTGAGAT	CGTGCCACTG	300
CACTCCAGTC	TGGGCGACMA	AGTGAGACCC	TGTCTCCNNN	AAGAAAAAAA	AAATCTGTAC	360
TTTTTAAGGG	TTGTGGGACC	TGTTAATTAT	ATTGAAATGC	TTCTYTTCTA	GGTCATCCAT	420
GCCTGGCTTA	TTATATCATC	TCTATTGTTG	CTGCTCTTT	TTACATTCAT	TTACTTGGGG	480
TAAGTTGTGA	AATTGGGGT	CTGTCTTCA	GAATTAACTA	CCTNNNGTGC	GTGTAGCTAT	540
CATTTAAAGC	CATGTACTTT	GNTGATGAAT	TACTCTGAAG	TTTTAATTGT	NTCCACATAT	600
AGGTCAACT	TGGTATATAA	AAGACTAGNC	AGTATTACTA	ATTGAGACAT	TCTTCTGTNG	660
CTCCTNGCTT	ATAATAAGTA	GAACTGAAAG	NAACTTAAGA	CTACAGTTAA	TTCTAAGCCT	720
TTGGGGAAAGG	ATTATATAGC	CTTCTAGTAG	GAAGTCTTGT	GCNATCAGAA	TGTTNTAA	780
GAAAGGGTNT	CAAGGAATNG	TATAAANACC	AAAAATAATT	GAT		823

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCTTTCCCA	TCTTCTCCAC	AGAGTTGTG	CCTTACATTA	TTACTCCTTG	CCATTTCAA	60		
GAAAGCATTG	TCAGCTCTTC	CAATCTCCAT	CACCTTG	GGG	CTTGT	TTTCT	ACTTTGCCAC	120
AGATTATCTT	GTACAGCCTT	TTATGGACCA	ATTAGCATTC	CATCAATT	TTT	ATATCTAGCA	180	
TATTTGCGGT	TAGAATCCC	TGGATGTTTC	TTCTTGACT	ATAACAAAAT	CTGGGGAGGA	240		
CAAAGGTGAT	TTCCTGTGTC	CACATCTAAC	AAATCAAGAT	CCCCGGCTGG	ACTTTGGAG	300		
GTTCC	TTCCA	AGTCTCCTG	ACCACCTTGC	ACTATTGGAC	TTTGGAAGGA	GGTGCCTATA	360	
GAAAACGATT	TTGAACATAC	TTCATCGCAG	TGGACTGTGT	CCTCGGTGCA	GAAACTACCA	420		
GATTTGAGGG	ACGAGGTCAA	GGAGATATGA	TAGGCCCGGA	AGTTGCTGTG	CCCCATCAGC	480		
AGCTTGACGC	GTGGTCACAG	GACGATTTC	ACTGACACTG	CGAACTCTCA	GGACTACCGT	540		
TACCAAGAGG	TTAGGTGAAG	TGGTTAAC	CAAACGGAAC	TCTTCATCTT	AAACTACACG	600		
TTGAAAATCA	ACCCAATAAT	TCTGTATTAA	CTGAATTCTG	AACTTTCA	GAGGTACTGT	660		
GAGGAAGAGC	AGGCACCACC	AGCAGAATGG	GGAATGGAGA	GGTGGCAGG	GGTCCAGCT	720		

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGATCCGCC	GCCTTGGCCT	CCCAAAGTGC	TGGGATTACA	GGCATGAGCC	ACCGCTCCTG	60
GCTGAGTCTG	CGATTCTTG	CCAGCTCTAC	CCAGTTGTGT	CATCTTAAGC	AAGTCACTGA	120
ACTTCTCTGG	ATTCCCTTCT	CCTNNWGTAA	AATAAGNATG	TTATCTGNCC	NNCCTGCCTT	180
GGGCATTGTG	ATAAGGATAA	GATGACATTA	TAGAATNTNG	CAAATTAAA	AGCGCTAGAC	240
AAATGATTTT	ATGAAAATAT	AAAGATTAGN	TTGAGTTGG	GCCAGCATAG	AAAAAGGAAT	300
GTTGAGAAC	TTCCNTTAAG	GATTACTCAA	GCYCCCCTT	TGSTGKNWAA	TCAGANNGTC	360
ATNNAMNTAT	CNTNTGTGGG	YTGAAAATGT	TTGGTTGTCT	CAGGCGGTTC	CTACTTATTG	420
CTAAAGAGTC	CTACCTTGAG	CTTATAGTAA	ATTGTCAGT	TAGTTGAAAG	TCGTGACAAA	480
TTAATACATT	CCTGGTTTAC	AAATTGGTCT	TATAAGTATT	TGATTGGTNT	AAATGNATT	540
ACTAGGATT	AACTAACAAAT	GGATGACCTG	GTGAAATCCT	ATTCAGACC	TAATCTGGGA	600
GCCTGCAAGT	GACAACAGCC	TTTGCAGTC	TTAGACAGCT	TGGCCTGGAG	GAGAACACAT	660
GAAAGAAAGG	TTTGTTCCTG	CTTAATGTAA	TCTATGGAAG	TGTTTTTAT	AACAGTATAA	720
TTGTAGTGCA	CAAAGTTCTG	TTTTCTTTC	CCTTTTCAGA	ACCTCAAGAG	GCTTGTGTTT	780
CTGTGAAACA	GTATTTCTAT	ACAGTNTGCT	CCAANTGNAC	AGAGTTACCT	GCACNNCGTT	840
GTCCNTACTT	CCAGAACATGCA	CAGATGTCTG	AGGACAACCA	CCTGAGCAAT	ACT	893

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCAGAAAATA	CTTTNGGGCA	CATGAGAACAT	ACATGAGAAC	AAGCTGATGC	ATAATTCCCTC	60
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CTGTGATGGA ATGTAATAGT AATTTAACAG TGTCTTTCT TTTTAACAGC CTCAAGGATA	120
CAGCAAAATA AAACAAAAGC AATATGAAGG CTGAGAATAG GTATCAGATT ATCATAAAA	180
GTATAGATCA AAAGGAATCT GGTKCTNAGG TTGGCGCAGC AGCCTCTAGA AGCGACNAGG	240
GAGACTTTA GAACTACCAT TCTCCTCTAT AAGTGGATCC NANGCCAGG RAAACTTGAT	300
ATTGAGNACA ATGGCCTTAC TGAAATAACC TGTGATCCAC TCGGNCTCAT CATCTCCACC	360
ACCACCATAA ATTTGATGAG TNCCTATAAT ATTCCANCCA GNNGAAATAC CTGGRAGGTT	420
ACTGAAAGGC NACNATCAGA CNAAAATAAA GNATACCGTA GGTAAATTCT ACAGT	475

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTTCTCNAGA TCTCTTCAAA ATTCAATTNTG CGCTATAGGA GCTGGGATTA CCGCGGGTGC	60
TGGAACCAGA CTTGCNCTCC AATGGATCCT CCANACNGGA NGGGGGGTGG ACTCACACCA	120
TTTACAGGGG GCTCGTAAAG AATCCTGTT TGANTATTNT NCCGTCAATT ACCNCCCCAA	180

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATGTAACMA CMAAACCYCA AACTCCTGNA AGAANATGGT TACTTATNGA TNCCATTNC	60
TTTTTNCACT CTCAGACATA AATATAAACM MANTTTCTAC TGTGGRAAAA CATCTNCAGG	120
GGNCNTTAN CCATGATCTC TAGNACNANG GGCTNGTGGN TNGTTTAAT GTCTCTAAGC	180
NACTNGACTA GTTTCTCTTN CACTGAGNAA ACTGCNACAA GTNNTTNCTN CTGNATCTGN	240
ACTGNAATGC TAAGTTNCAA GTNCCAATGA GCTNGTGANT TANYCTTTAT TTNAMCNAAA	300
GTNNNTTAATC ANCCNCAGTG TTACTTTGNA AAGCTNCTCC CTGGACAGGC GGCCCNACTT	360
CTAATGTTAT GAATGGGCTG GAGNANCCTC NACNTGAGTT TNNWAAGGNT CAACANCCAA	420
TRGNAANTGT AMCCGACTCT AAATTCCAAC CNATAAT	457

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCTGTGCTA GGTAGTGTAC TAATCATTCA GTTTATCTCA TTTAATCTNN ATGNAACTCT	60
AAGTCATTG CTNTGANCNA CACATAACAG ATCTCGCAAC TGNAGTTAG CGAGGCCAGT	120
TAATTTKCCA AAGNTCATAA TNCTAAGNAG TTCTAGNATG GAGATTCTMAA GTCCNACTGT	180
TTAGTCAAGA GACCCTACTG TTAACTAGTA CCTTTACACT ACTAACTGGG TAANCCATAA	240
NCAATTAATG ATAAAAGATTG AGATTACTKC CACATTCTCA CTGGTTATAA ATTAAAACNT	300
CAAATAAAAA NTCTTGGCAC TTCTATGGTA ATATTTTAT TAGGATAAAC TTTCAAGNAG	360
TGGATNCTAG GTG	373

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCACACTGN TGGGCCATGG AAGCCATGAG TGTACCACAT GGCCCTGTCC CACTGGCAC	60
AGTNGATTGG TTGGNTCGGG AGTAGTCACC TGATTCAAGN TGGCCAATC AGATCCTACC	120
TCCANGGGGT TNGGAATTAG AAAACAGTGA CCCTAGYTAG TNTAGGCNAC TTGAACTGGA	180
GGGCCCATAC ATTCAAGGAGC CTTATGGGGC CATGTACACA TGGAAGCAGG AAGANTGAAG	240
GAGGGAGAAG TAGAGGCCAG AAACCCACCT GGGTTCTGT TTCCCAATGN TAAGTCCCTG	300
CCATGTYCCT GCTCTTCCTG TGGTTNGGAT CTTCAAAGGT TGCTCAAATT NGGGGCAGTG	360
GCCCTGGCAG CTTTCAAAT CCTYCCCATT TTTATTGAAG CTGAAAGACC CTTGACTAGA	420
AC	422

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATTGTTATTT	TTCGTCACTA	CCTCCCCGGG	TCGGGAGTGG	GTAATTGCG	CGCCTGCTGC	60
CTTCCTTGGA	TGTGGTAGCC	GTTTCTCAGG	CTCCCTCTCC	GGAATCGAAC	CCTGATTCCC	120
CGTCACCCGT	GGTCACCATG	GTTAGGCACG	GCGACTACCA	TCGAAAGTTA	ATAGGGCAGA	180
TCTCGAGAAT	TCTCGAGATC	TCCNTCMAAT	TATTACTTCA	NTTKCGGTAG	TGATCAGNAC	240
NAGGCAGTTC	TATTGATTTC	TCTCCTTCA	TTCTGAGTTT	CTCCATAAAT	TAATTGGACC	300
TAATCATGTT	TKNAATCCTG	TCTTTAGGG	GGNANTTGNA	CTNTCAAGTG	TTTAAAGGGA	360
GGGNCGGAGN	ATGATTNTGG	ATTGGAGTGA	GAGCA			395

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGANTTCT	GGGTNAAAAG	GACCTNANAC	ATAATATAGT	GGACTTNCAA	TAAACACTTA	60
CCAAATGGAN	AAATGAACCC	CTGGTCACCC	CGATCTCACT	AGTNCTNCC	CTGAAACCCG	120
ANANATCTGA	GTCCTTTCT	CCTTTACTAA	CCCTTNCTCC	AATCCTGCTC	ATGGGAATTAA	180
ANGNTGTAAA	ATANGCCTGG	GGNACCTCGG	RCCTCTNCCC	TGGGNTCTGT	GGGTGGGAGN	240
ACTGTGGAAG	CCGTWTCAAT	CGCCCCCACC	TATGAGAGCC	TTTCTNCAGG	GCCAGCCATG	300
AACGTCCCCC	ATGTNATCAG	NATCTNCAGG	CTACTGCTGT	CCTTCYTGGA	TWTTTAACCT	360
GGRGGCGGGC	CAGGGACAGA	AAARGGAGGT	GGCAAGATCC	TTGAACAAAA	GGAGCTATAA	420
AAGGGCGTTG	GGGGAAGCAA	GGCAAACGGC	AGATTAAACA	AGCAGGCACC	TCAAGGAAAC	480
GTGACGC						487

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCGAGATCT	GGCCCATCAT	TTAGTTTAT	NGCTTGNAGT	NTNTAGNAGA	TAAAACATCC	60
ACGTGGATCT	NCTCTTAGAG	AAATCAANTA	CTTTAGGNAT	NTGATAGTCA	GAGANTGGNT	120

ATCAAATNGA AAGGNATNTN GGTNGANCAG TTAGTTNGYN CCNTTNGNNG AGACCACTGG	180
GNTGTNGASA CCAGATTCMK GGGTNCNAAT CTTANGTAA TCTNAGAGCC AACACATGGG	240
TCATNTTATS CCCCCAAACTT AGCCACATCT BGTGGGGYTA TGGNGTCACC CCAAGAGCAG	300
GAGGAGCATG GNTGGATGGA AATCCATCTC CACCACTGGA ACCCCAAWTT CTGAATGNAT	360
CACCTGTTAG AGTTTCTTGT YCATAAAATA GCAGGGAATT TAGGAATTAA GTTTTTTTT	420
AATAGTTGG GCCTTTATC CACACTCTCA GGAGCTTAGG ATACTTTCT CCTTCAGCTC	480
ACTCTGAAAC TCCCTCTGGA	500

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCGAGATCTG TGGTAGTNAC ATGATATTCT GGCAMCTACT TTCATTATCA CCTTTATTAA	60
AATAAATTAA AAGAAAAATG GCAGTATGTT TCTGTGRAGN CCACGAGTAC TCATTTAAA	120
GGACTCMAGA GTTNCAGRNA AGTAAAAAGR AAAGAGTAAA ATCATTCTT AANTYTYWYY	180
TTCCAGAAAT AACGATGTTG AGCATTAAGT GGACTTCATT TCATACTCTT TCMMAGNTTA	240
TGTAGGCATA WAWATGTGTG TGTATATACA TATATATGGG TACATCCTTA GAGAAGTTGG	300
CTGGCTAGAT AGACACACNT NAAAAATGGR ATCATACTCT AATKCCATT NNANTTTANA	360
AAATACATAT TCAGANCCNC TGTNCTTATA NACAGAGTAA NTGAAA	406

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GACCCAGTAA AACTTATCTC ATGAGCATAA GGCTGAATGG GATTGACAGC CTACAGAAC	60
CGGATTTAT CATGAGGGCA TTAGTGGGG TTGGGGGTTA GGTACTGAAA GTTTAAGGAG	120
GTGAAAGGAA AGCAACTTGT GCCTTACAGG GTCAAGCTAG GTCAAGGAAA TTCCCAGGAG	180
CGTGTGGAAG CTCTCTACCT GATAGGTGAG CTCAAGCTTA TGACCGCCCA AGCTTCTCCC	240
CAAGCTTCCC TTCCACTGCT TCCTCTTGAT TGACTTCCAC AGCAAGGTC	289

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATCAGGAT TTACTGAGTA AAAATCTCAG GTNTTAACCA TGCCCCTAAA ATGTGCTATN	60
CCAAAGAGGA ACAGGTTACT TGGGAGGAAA AAAGCTGCCT GGGNAACTCC CCNCAAATGT	120
TTATTTAAA TAAAAATGGT NGATGGAAAT ATTTNTAAA AGAACTTGGG GTNTAATATG	180
GNATACTGCC CATCAAACAA AAAAGGAAAT AAAACTTCNT TCCCATTAT AATAAGTTNC	240
CCACCCTTTA CTATCAAGAT TACAACTTAT TGACCTTTA TGCTNGCTNG GTTTTTTGG	300
GACTGCCTAA TCCAATGTTT AAATTTCTA NGTCTGNATT TCAATGTGGG TAGGAGTNAT	360
TTTCAA	367

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGTATCTGA CAGGTAAGAT TGCTTTTAA AGTTGTTTA AATGCATTAC ATGACTGAGA	60
AAAGAAAAAT GCACATTTA TTGTTGCAGT TTAAAATTTC ATTTNGNGTG AAACTAAACG	120
TGAAACAAAA GGGATAAAATG TGTTTGNTT TTGTTTGTT TTTACCTGTT TGGGGTATT	180
TTTTCTGAGT TTGTGTAGAA ACCCGTGTGG NTACACTGGG TAATCTGTC AGGGNTACMA	240
AMCTTGGGTC TTGANTTTGG TTANTTGGNT TTANTTGGTG NACCCATGTA CTTGCTCTTC	300
CNTCCCAGAA ACATAGCTTG GTAGGCNAGG GTTAANCCAG TGTCGGCGAN CCCATGTCCC	360
TANCACAGCA TCTTGTAAGT TTAATGCACA ATCGTTCCNT CCCAGGATGG ANTTATCATT	420
ATAAA	425

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGAGGCAGCA GGAGCCACAA ATAAAGCAAG AGCCAGAAC AGAAGNGGAG GAAGAAGAAA	60
AGCAAGAAAA AGRAGRAANA CGAGAAGAAC CCATGGRAGA GGAAGAGGAN CCAGANCMMAA	120
AGCCTTGTCT GAAACCTACT CTGAGGCCCA TCAGCTCTGC TCCATCTGTT TCCTCTGCCA	180
GTGGNAATGC NACACCTAAC ACTCCTGGGG ATGAGTCTCC CTGTGGTATT ATTATTCCCTC	240
ATGRAAACTC ACCAGATCAA CAGCAACCTG AGGAGCATAG GCCMAAAATA GGACTAAGTC	300
TTAAACTGGG TGCTTCAAT AGTCCTGGTC AGCCTAATTG TGTGAAGAGA AAGAAACTAC	360
CTGTAGATAG TGTCTTAAC AAATTTGAGG ATGAAGACAG TGATGACGTA CCCCAGAAAAA	420
GGAAACTGGT TCCCTTGGAT TATGGTGAAG ATGATAAAAA TNCAACCAAA GGCACGTAA	480
ACACTGAAGA AAAGCGTAAA CACATTAAGA GTCTCATTGA GAAAATCCCT ACAGCCAAAC	540
CTGAGCTCTT CGCTTATCCC CTGGATTGGT CTATTGTGGA TTCTATACTG ATGGAACGTC	600
GAATTAGACC ATGGATTAAT AAGAAAATCA TAGAATATAT AGGTGAAGAA GAAGCTACAT	660
TAGTTGATTT NGTTTGTCT AAGGTTATGG CTCATAGTNC ACCCCAGAGC ATTTTAGATG	720
ATGTTGCCAT GGTACTTGAT GAAGAAGCAG AAGTTTTAT AGTCAAATG TGGAGATTAT	780
TGATATATGA AACAGAAGCC AAGAAAATTG GTCTTGTGAA GTAAAACCTT TTATATTTAG	840
AGTTCCATT CAGATTCTT CTTGCCACC CTTTAAGGA CTTKGAATT TTCTTGTCT	900
TKGAAGACAT TGTGAGATCT GTAATTTTT TTTTTGTAG AAAATGTGAA TTTTTGGTC	960
CTCTAATTG TTGTTGCCCT GTGTACTCCC TTGGTTGTAA AGTCATCTGA ATCCTTGGTT	1020
CTCTTATAC TCACCAGGTA CAAATTACTG GTATGTTTA TAAGCCGCAG CTACTGTACA	1080
CAGCCTATCT GATATAATCT TGTTCTGCTG ATTGTTTCT TGTAATATT AAAACGACTC	1140
CCCAATTATT TTGCAGAATT GCACTTAATA TTGAAATGTA CTGTATAGGA ACCAACATGA	1200
ACAATTTAA TTGAAAACAC CAGTCATCAA CTATTACCAC CCCCACCTCTC TTTTCATCAG	1260
AAATGGCAAG CCCTTGTGAA GGCATGGAGT TTAAAATTGG AATGCAAAAA TTAGCAGACA	1320
ATCCATTCCCT ACTGTATTTG TGTATGAATG TGTTTGTGAA TGTATGTGTA AAAGTCTTC	1380
TTTCCCTAA TTTGCTTGG TGGGGTCCTT AAAACATTTC CCAACTAAAG AATAGAATTG	1440
TAAAGGAAAA GTGGTACTGT TCCAACCTGA AATGTCTGTT ATAATTAGGT TATTAGTTTC	1500
CCAGAGCATG GTGTTCTCGT GTCGTGAGCA ATGTGGGTTG CTAACGTAT GGGGTTTCT	1560
TATTAATAAG ATGGCTGCTT CAGCTTCTCT TTTAAAGGAA TGTGGATCAT AGTGATTTT	1620
CCTTTAATT TTATTGCTCA GAAATGAGGC ATATCCCTAA AAATCTCGGA GAGCTGTATT	1680
TAATGCATT TTGCACTAAT TGGTCCTTAG TTTAATTCTA TTGTATCTGT TTATTTAACAA	1740
AAAAATTCAAT CATATCAAAA AGTGTAAAGTG AAAACCCCT TTAAAACAAA ACAAAAAAAT	1800
GAAATAAAAT TAGGCAAATT GACAGACAGT GAGAGTTTA CAAACATGAT AGGTATTCTG	1860

CTCGGCAATT TGTAAGTTA CATGTTATT AAGGATAAAG GTAAATCATT CAAGGCAGTT	1920
ACCAACCAC AACTATTTGT TTTCATTTT GTCTTGTAGA AGGTTATAT CTTGTTTAC	1980
CTTGGCTCAT TAGTGTAA AAATGTACTG ATGATGTGCT TAGAGAAATT CCTGGGGCTT	2040
TCTTCGTTGT AGATCAGAAT TTCACCAGGG AGTAAAATT CCTGAAAACG TAAGAAGTTT	2100
TAAACAGCTT TCCACACAAA TTAGATGCAA CTGTTCCCAT GTCTGAGGTA CTTATTTAAA	2160
AGAAAGGTAA AGATTGGCCT GTTAGAAAAA GCATAATGTG AGCTTGGAT TACTGGATT	2220
TTTTTTTTT TAAACACACC TGGAGAGGAC ATTTGAAAAC ACTGTTCTTA CCCTCGAAC	2280
CTGATGTGGT TCCATTATGT AAATATTCA AATATTAAAA ATGTATATAT TTGAAAAAAA	2340
AAAAAAAAAA AAAATTCCCTG CGGCCGCAAG GGAATTC	2377

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATTGGAGCTC CACCGCGGTG GCGGCCGCTC TAGNAACTAG TGGATCCCC GGGCTGCAGG	60
AATTCTCGAG ATCTCCCCA AGTAAATGAA TGAAAAAAAG AACAGCAACA ATAGAGATGA	120
TATAATAAGC CAGGCATGGA TGACCTTATA GCACCCGTGA TTTATACAGA ACCACCAGGA	180
GGATAGTCAT GACAACNATG ACACGTGATCA TGATNCCAGC ATTCAGAATT GAGTNCAGGG	240
CTCTCTGGCC CACAGTCTCG GTATCTCTG TGNATGGGT ATAGATTARC TGTCCATCCT	300
TCCGGGNATA AAANCTGACT GACTTAATGG TANCCACGAC CACCACCCAT KCAGAGAGTC	360
ACAGGGACMA AAGAGCATGA TCAACATGCT TGGCNCCATA TTTCAATNTC ANCTCCTCAT	420
CTTCTTCCTC ATCTNCTCC ACCACCTNCC GGGAGTTAAC CCTGGGGTCG TCCATTAGAT	480
AATGGCTCA	489

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGGTGCTTC AGTGTGGCTG ACACAGCAGC ATGGTCTTGA CAAGTTTCT TCATCCTACC	60
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ACAAAATCCC AGTTGGTAAT AGAGACTTTA CTCCTACCTA TCAAAACCAC AAAATGTCCC	120
ATTAGGGGG GACATGTTGT ACATGTTAGG ATCATTCAA TAACCAAGAT TATAAGGTGA	180
GGAAAGATGC CCCTAACTGA TTCTTTGTC TCTCATCTTG TTGGTCCAG GGACCGAGTG	240
GGGTCAATCT TCTGGTSSTG CCTCTCCAGG TCTCTTCCAG GCCGGTCATA GACGTACTCC	300
CTCTGAGGCC GACCGATGGT TAGAAGAGGT GTCTAAGAGC GTCCGGGCTC AGCAGCCCCA	360
GGCCTCAGCT GCTCCTCTGC AGCCAGTTCT CCAGCCTCCT CCACCCACTG CCATCTCCCA	420
GCCAGCATCA CCTTTCCAAG GGAATGCATT CCTCACCTCT CAGCCTGTGC CAGTGGGTGT	480
GGTCCCAGCC CTGCAACCAG CCTTTGTCCC TGCCCAGTCC TATCCTGTGG CCAATGGAAT	540
GCCCTATCCA GCCCCTAATG TGCCTGTGGT GGGCATCACT CCCTCCCAGA TGGTGGCCAA	600
CGTWTTTGGC ACTGCAGGCC ACCCTCAGGC TGCCCATCCC CATCAGTCAC CCAGCCTGGT	660
CAGGCAGCAG ACATCCCTC ACTACGAGGC AAGCAGTGCT ACCACCAGTC CCTTCTTAA	720
GCCTCCTGCT CAGCACCTCA ACGGTTCTGC AGCTTCAAT GGTGTAGATG ATGGCAGGTT	780
GGCCTCAGCA GACAGGCATA CAGAGGTTCC TACAGGCACC TGCCCAGTGG ATCCTTTGA	840
AGCCCAGTGG GCTGCATTAG AAAATAAGTC CAAGCAGCGT ACTAATCCCT CCCCTACCAA	900
CCCTTCTCC AGTGACTTAC AGAAGACGTT TGAAATTGAA CTTTAAGCAA TCATTATGGC	960
TATGTATCTT GTCCATACCA GACAGGGAGC AGGGGGTAGC GGTCAAAGGA GCMAAACAGA	1020
YTTTGTCTCC TGATTAGTAC TCTTTCACT AATCCCAAAG GTCCCAAGGA ACAAGTCCAG	1080
GCCCAGAGTA CTGTGAGGGG TGATTTGAA AGACATGGGA AAAAGCATTG CTAGAGAAAA	1140
GCTGCCTTGC AATTAGGCTA AAGAAGTCAA GGAAATGTTG CTTTCTGTAC TCCCTCTTCC	1200
CTTACCCCT TACAAATCTC TGGCAACAGA GAGGCAAAGT ATCTGAACAA GAATCTATAT	1260
TCCAAGCACA TTTACTGAAA TGTAAAACAC AACAGGAAGC AAAGCAATGT CCCTTGTGTT	1320
TTCAGGCCAT TCACCTGCCT CCTGTCAGTA GTGGCCTGTA TTAGAGATCA AGAAGAGTGG	1380
TTTGTGCTCA GGCTGGAAC AGAGAGGCAC GCTATGCTGC CAGAATTCCC AGGAGGGCAT	1440
ATCAGCAACT GCCCAGCAGA GCTATATTT GGGGGAGAAG TTGAGCTTCC ATTTTGAGTA	1500
ACAGAATAAA TATTATATAT ATCAAAAGCC AAAATCTTA TTTTTATGCA TTTAGAATAT	1560
TTTAAATAGT TCTCAGATAT TAAGAAGTTG TATGAGTTGT AAGTAATCTT GCCAAAGGTA	1620
AAGGGGCTAG TTGTAAGAAA TTGTACATRA GATTGATTAA TCATTGATGC CTACTGAAAT	1680
AAAAAGAGGA AAGGCTGGAA GCATGCAGAC AGGATCCCTA GCTTGTGTTG TGTCAGTCAT	1740
TCATTGTAAG TAGCACATTG CAACAACAAT CATGCTTATG ACCAATACAG TCACTAGGTT	1800
GTAGTTTTT TTAAATAAG GAAAAGCAGT ATTGTCCTGG TTTTAAACCT ATGATGGAAT	1860
TCTAATGTCA TTATTTAAT GGAATCAATC GAAATATGCT CTATAGAGAA TATATCTTT	1920
ATATATTGCT GCAGTTCCCT TATGTTAACAT CTTAACACT AAGGTAACAT GACATAATCA	1980

TACCATAGAA GGGAACACAG GTTACCATAT TGGTTGTAA TATGGGTCTT GGTGGGTTT	2040
GTGTTATCCT TTAAATTTG TTCCCAGAG TTTGTGGG ATGGGATTC TGGTTTATT	2100
AGCTTTGTGT GTGTCCTCTT CCCCCAAACC CCCTTTGGT GAGAACATCC CCTGACAGT	2160
TGCAGCCTCT TGACCTCGGA TAACAATAAG AGAGCTCATC TCATTTTAC TTTGAAACGT	2220
TGGCGCTTAC AATCAAATGT AAGTTATATA TATTGTACT GATGAAAATT TATAATCTGC	2280
TTAACAAAA ATAAATGTTC ATGGTAG	2307

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCAGCTATT TACATGGCCT CACAGGCATC AGCTGAAAAG AGGACCCMAA AAGAAATTGG	60
AGATATTGCT GGTGTTGCTG ATGTTACAAT CAGRCAGTTC TATAGACTGA TCTATCCTCG	120
AGCCCCAGAT CTGTTCTTA CAGACTTCMA ATTKGACACC CCAGTGGACA AACTACCACA	180
GCTATAAATT GAGGCAGYTA ACGTCMAATT CTTGANNACM AAACTKNCC TGTTGTACAT	240
AGCCTATACM AAATGCTGGG TTGAGCCTTT CATAAGGNA AACMNAAGAC ATGGNTACGC	300
ATTCCAGGGC TKGANTACTT ATTGCTTGGC ATTCTTGTAT GTA	343

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAGGGCTAA CCAGCCACTG CACCAAAATT AGTCCTTACA TTATAATACT CTGGCCATTG	60
GAAGAGAAAA ATGGGAAAAT TCAACAAATT GAAAGACTAT GATCCCTCTG GCTCATGATC	120
TACTGACCAAG AATGAAGTCC TGAAGGATTT CCTTCTGTTA TGTTATCTAC CCAGCTAATC	180
TCAAACAAGA GGAGCTGGAA AGAACAAAGC CCCATGAAGC TACCCCTAGA CCCAGAAAGC	240
CAAGAACAGG GCCAACAGAAA TGAACAGCAG ACAAGCCTGA AATAGAAGTG GNACAGACAT	300
GTGGNAAGAC CAAGTACACC CAGTTNGGTG GTAAAGATTC CGATATCAAG CTTATCGATA	360
CCG	363

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGTACATGGT TTCTGNCCA	CCCCASCCAC	CTTCCCCAT	CTCTACCGGY	TGATAGTCTC	60
TCAGNTAGTA GACCTTTCT	NGTTTAGRCA	GGGCACNTT	TTTAAAAACT	CCAGACGGGT	120
ACCCCTCCATG TKGMAGGCCA	CGTGGCCCTG	GATCACTCAA	CTGANTGTCA	TNKGANTGGT	180
GCCCCCAGAG TGAGGACAAT	GGTGNAGCCC	TCCTAAGGCC	CTNCCTGAGT	GTCCCTCCTT	240
CATGAAGATG ATTCTGAGGN	TTCCCAGGCC	TNCACCCTTC	TTKGAAARCC	CATAGNAGTT	300
CATATGNACT NCTCTNCTAT	GCTCACCAAA	CTCTNCCTTC	ATCATACTTG	GGGGATGTGT	360
GT					362

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GTGCATGTAA TTACAGTTAC	GATATATGAA	ACGTACAAAA	TATTATGAGT	ATATAATATG	60
GGGAGACTTA ATCTAGTTG	GGGGATCAGG	GCACATTCT	CTAAGAAAGT	GACATTGAA	120
TTGAGCTCTG AAGGATAAAAT	AGACATTACC	CAGAAGAATA	AAATGATGGG	GAAGAAGGAG	180
GACATTTCC GTAGATTCC	AGTGGCCCCN	CTTGATCCCT	TATCCACTCA	TCACTNAGGA	240
GGATATTAAA TKCTATAGAA	ATGGRAGRAA	GACMMAAAGA	GACCCTNATA	TCTCGAGAGG	300
ATCCAGCMAA ATTCCAAGAG	ACACAACAWT	AAGAAACTNG	GAAGGAAGAG	AAAAGGCMMN	360
NNAGGNAAAA GAAAGACAAG	GAAATTNWNN	NAGNACGGAG	AGAAAGAGAG	AGGGAGCGTN	420
NAAGGGNACG AGAAAGGCAG	GNACGGGGAC	GAGAAAGGGN	AAGAGNACGT	AAACG	475

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGAAATAAAT GAGATCTCAG TGGTGGTATG GATTGGACTG ATCTCTGTAA CTGTGTNTGG	60
AAAAAGGACC GGAAAATGAA AGCCAGATCC CAGTAAGGGG TAGAGAGGGG CCAAGAGAAC	120
TGAACATCTG GGCTGCCGGA GAAATCAAAG TCTAGGAAGT AAGAGGTAAG AGTGTACTAC	180
AGGGGACATA CCCCAATCTC TTGGTTCCCT CCCTCTNCCT TCCTCTCCCA GAGACCCAGG	240
TCCCTGGGAC TATNTTGGAT CTGTCTCTGA AGCTGAAAAA CAAAAGGCAG AGGAGACAGT	300
CGGNTCTAAG TGACCAATCT CAAGCCAGCT TGGTCAGAAN TCCTAA	346

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAATCCAGTG CAGGCAACAT TATGTGGAAA TAGAACAGG GCTCCTGCTA GGAGATTGAN	60
ATTCTGGCTT TCCTTTGGAA CCCCTCACTG ACTCATCGCC CCTGAANCAG GANCCANCAG	120
GTNCCAAGGC TCCCCCTGCTC CTNTCCCTNC CCCAGGGCGA GATAGGAARC CGGAARCCCTG	180
GGCAGGGCTGA RCCCANCCGA CTGGAACCAAG GGNAGANCCT GTGGGTGGGT GGNAGGGAGG	240
GAAGGAGGCC AGATTCCCTCC AGAACTGGGG RAGAGAACAG GTTTGGAAG TTGGGGGAGG	300
GTTTGGGTTT CACAGTGATG GTTTCATGAN ACCCTGGAGG GTTNCACACT CCTGGTKCAN	360
TTTTGNTANT CGTNCTTTGA ANACARNCCG CTTCCCTTCA ACCCTCCNCN TAAAAAGTTT	420
TGATNTTTA AGG	433

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACCAAGAGCC CCCAGTTAT GNTAACTCTC ATGACAAACA CAATTTAGT ACCTCTCACT	60
ACCAACTATC CAGGAACCAAG GANTCACCTA TTACTACGGT TCCAGCAGAA TGGGAATCCC	120

ATTCTCGGAT ATCCAGGGTA AATCCCTGAC CATGTGAGAG GAATCCTAGT GCCCCAACAA	180
CCTCACCCCC TGACTCCTCC TCAANGGCTC TGCCAAGTCA ACAAAAAAAAT CCTCTACATT	240
TACACTATCT GTAAAGCCAA AGACCAGCGT CAACCTAAAT GTCCATCAAT AAGGGAATGG	300
TTGGATAAGT AAAAATTATG CAGCTGTAGG AAGGAATGAA GAATGTCTAT	350

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAAGGGAACA AAAGCTGGTA CCGGGCCCCC CCTCGAGGTC GACGGTATCG ATAAGCTGGA	60
TATCGAATCC TCGAGATCTA CCTAAAAAAA AAAAATTAAC TTCCCAAATG TGGGAGTCTA	120
CTCTGTTCCC TCCTNGTNTT TATTNCTGTN TACTTTYCTA ANATGGTTAA AATGTGTAAN	180
CAATATGTGT CCTTNACTN KGGKGTGAAC ATTTTYCTA TTATAAATYC TWAGAAAATA	240
TTNCTATGGN TATGAGATAT TKGATTCAA GTGCCTKGTA ATTTACTYCT CAAATGTCCC	300
TGATGKGGA NATKGTTNC TAGTGTYYCA CTATTTAAAA AAACAGNAAT ATCTGTCTNT	360
ATGCTNAGAG CTTNTYCACT TTYCAAATTA TTNCCTTAGG GTAAAATCCT AGAAGTAGAA	420
TTTTGGGGC AAATTATCTA CATATTTATA ATTGTCTTGG TATTCCAAAT CTCGTTTCC	480
AAAAGCTTAT ATCAATTGT ACTTAACACC AG	512

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATTTAAGATG ACTGGGGGTC TCTNCCTAAT CCCATACTCC ACTGGAGAGG ANAAGTGGGA	60
AAGGTTGGTC TAGTTARGGT NGNTGGGGAC CCTCCCAAGA GCTGNAGAAG CAGAGATAAG	120
NAGAGCCTNC TNCTAAATCC ACATGGNCCT YCCAAGGNTC TCATCCTCTA GGACCTACCA	180
CTNCTCAGTC TACTTACTTG TCTYCTGANA TGCTTTCTNG AGGGGNAGAA AACAAAGGAA	240
GAGTAATAAC AAGCAGNAGA AACTGCAGAG AATGNAAAAT AAGTCCATAG GAGAATGTTG	300
NAAATAGAAT CATCCNCCTT TACATATTGT CACTCCAGGA AAACTGCCAA GAACCACTCA	360

TTCCTCTAGA TACAMTTCT GTAGGATCCY CCCAGACTTC CTCCCTTAAG CACGTCAGTA 420
TTCTCCTTAT TCTCCCTTCA TTTCAACCCCT 450

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 766 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGAGATCTGC CCCAGCCCAC ATTCCTTTG TTGAATGAGT AGAGAAGACT GAGAAGTATC 60
ACTCACCCGT GATGTGGTTT GTCCCTTTTC CAGCCAGTGT GTTGGTAATA AAAGTCACCT 120
TTCAGAGCTT TGGTCCCCGT AATGCCCGTC TTTCCTGTGT CCAGGAATAA CCTTGNTAC 180
TAGGCAGTCC TCTGAAAGAT TTGTAGAAGG TTAAAGTGGA AAGGGACTTG GAAGCTCATA 240
GAATCCATGC CTCTTCTTT AGCATCAAGG AATTAGAAGT CCTGAGAGAT GAAGAATGTT 300
GTCTTCCCAA CTCAAACCCA TTTCTTGAAG CCATTTCCCT GGTTACTGNA TTGGCCACAA 360
CCCTTCCCCC TTGNTATCCT CATCCTGCTA ATGCTGTTT TAATGGCCTG CCAGTCTGGA 420
TTTGTCTTG GCAACCAAAC AATTTGCTT CACAAGATTG CTACTTAAGG GAAGAGAGGG 480
GCTCCTCATT TNTCACTTGT ACAAGAGCAG GGCTGGTCAG CTTTACACAG GTGTCAGATG 540
AACCGTCACA ANCCAGANTT NCATGTTGGC CTCAGGAGGG CTTCNAGGTC CAACATCTCG 600
ACGTAAGGAG CGTTCCCACT TCTTCATGC TCAGATAACA GTNCTAACTN CAGCTGTTTC 660
ATCCCNAATC CCTANTTGAG GTCTTAACAT CTATTCCATT TTKCCNACMA GGGTTATNCT 720
GTTAACCCCTC TNCACCAGAN TTAGANCTGA CTGATNCACT TCCTAG 766

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCATACTTGT ATAGTTCKNT AAGATAATCA CTCTCTCACT CAGACATNNG GNGRARNGCC 60
CNTCGATCAC TTGGGANAGG NGACTTGCMA TGTTTAATGA TTGTCANCCM NANAANTAAAG 120
CTNACAGGGC AAAAACAGCC TYANGTCAGT TCTNTCTCCC TAATCCTCTA GRAKNAAATC 180
NNAWRNTRNN ACTCTGNNTC TGTGCCATNA NANATNTTNC ANTTGTATTT ATGNACTCCA 240

CATNGAGTAC ACCTCACTAA WTNTNCTNCT GGGNAACNCC CSCMCANNTT TTTNNNTTGNT	300
GANANACARC AATGCTGGCA TACNGTG	327

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCAGACTTTC ATAACCTNGTG TTATTATGAA GATTAGAGTN CTGAAGCTTA CTGGATTAGA	60
AGAGNACGAG GGGGTAGCTG CCCCAATATA TTCTAATTTC TCTKGAGGAC CACCAAATNG	120
GMAGAGTGTGTC TCTGATAGGG AAAAGGAAGA GTTGGAAAGGN ATCTTAGCCT CTAGGANAAA	180
AGAACCATTT TTATTGGCCA CCAAAGTTAC ATCTAGTKGC CTACAAATTT ATNTCCAAAC	240
TCCTTATCCT GCCAATTCAAG GGTCCCTGNAA ACTGATGCCA AACTATAGTT TAGTCTNCTA	300
TCACATGACT GCATTATACA TACCCAATTA TCTGGGMAAA CAGACCTGAT CCAAACACAG	360
TTKGGTNCTT TCCTTNCCCTT NCCTKGTTT AGCCTGTYCC GTCTACTNGG GGTGTCTKG	420
ATTTGCTCCA G	431

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTTTTTTCCA CCAGACTTAC CAAATTTAG ATGNATGGAA GAACTGTAAA TNCCCATAAA	60
GNTAATCTAT NCATNGACCC CCACCATTAT GATAGAGATC ATNTGGTGAN TAATGAAAGA	120
TGAAACTCTC AGCTGGAAA GTAANAAGGA ATAGGATGTA AGTATGAGCT CCTGTTTTT	180
ATTATNTTTA TGGATGCCCC CTCAGAAAAA TATGNAANGG GGTAAC TGAC TNGGAAATGG	240
GTNTTTTATG NATAGTAAGT CCCACTCACG AGGTTT	276

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCGAGATCTA AAGCAGATGN AGACTTNCA CNAAATAAAT TTACTGCTTT TTYCTGTGA	60
NATAAGTTNC GAGAAGGAAA GCTTTKGATT NCTRNATGAG TYCAGTGGAT TATYCTNAGN	120
ACTAGAGTKG NKGTKGAGN CATGGNACAT TTATATAGWT YWTCAGTTC TACACTAAAT	180
GATGGAAGAA TGAGAAATCC TATATGACAA ATAGAAAAGT YCATYCTYCA TAATTGAGAA	240
CATTGAGCAG TTGGATTACC AAGATCTCGA	270

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTAGTTTA GACTAGTTTC ATTATACTAC CAGTTCTAA TATGTTGGTT TTTTATTAC	60
TATTTGATAT ATTTGTTTA ATATATGTT TC TTGTTTAGC AGGTAAAAGA ATCATAACAA	120
ATGTTTTAA AAGAACATTA TTATTCTTA ATAACGTCT TTTTATGCAT TTGGCATGCC	180
AACTTTTTC ATTAACATCT TGGGTATTT ATAAAAAGAG GGAAAGCTCA ATGTTAACAA	240
GGTAGCTTT CTTAGGAGCT AAATTAATA TTTAACAAAT CTCCTCCCT TCNCCTTCC	300
CCATCCCTCA AAGNATGGGT GNANTTATCT TTAACTTTG GGCTNGCATC CNTGNAAGCT	360
TATGGNTANT CATAGTCTNA CMAAACTAGG GTCACCNAAC TTGGCAGCAG AAATAATCTA	420
GTCTTACTGT GATAACTACC CAATTACTTT ATTATTTTC CAGTTNCAGT TCCAAATGTT	480
TTGTGGNAAN AATTTTNCT GTTTGTGATT TTCCAAGCTT AGAGGGGAA ACCAACTTTC	540
CAGTGTGGA GAGCACTGNA TAGTTATGN ATTGTGTAAA	580

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGTTTCTTAA NACAGAAAAA AATTTACTGA TNGGACATTG TTCTAAGTGT ATTATTGTAT	60
TAAATGGATC ATTTAATTAA ATCTTCATAA CTGACATAGG AGTTGAGTAA CTTGTGTGGT	120
CAAATAGCTA GTAAGTGATG AGTAGGCTGG GCGCAGTGGC TCAAGCCTGT AATCCCAGCA	180
CTCTGGGAGG CTGAGGCAGG CAGATCACTT GAGGTCAAGGA GTTTGAGACC AGCCTGGNCA	240
ACATGGNAAA ACCTCGTCTC TACTAAAAAT ACAAAAATTA GCTGGCGTG GTGGGNGCGC	300
ACTTGTAGNC CCAGNTACTC GGAAGGCTGA GGCAGGAGGA ATCGCTT	347

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCTCATCATG CTTCACGGGG GAGGCTGTGC GGGAAAGAATG CTCCCACACA GNATAAAGAA	60
TGCTCCCGCA CAGGATAGAG AATGCCCG CACAGCATAG AGAAGCCCC GCACAGCATA	120
GAGAATGCC CCNCACAGCA TAGAGAAGCC CCCGCACAGN ATAGAGAATG CTCTTCACCT	180
CTGGGTTTT AACCAGCAA ACTAAAATCA CAGAGGGCAA CACATCATT AAGATAGAAA	240
TTTCTGTATC TTTAAATTTC TTTCAAAGTA GTTTTACTTA TTTNCAGATT CTATTCTTT	300
ACTAGAATTA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACAAACAAAA	360
GCTAGGTTTT NTNCATAGGT CTNCTTCNN ATTGAATGAA CGTCTNTCCT CAAATTANC	420
CCCCCAGGGA	430

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CAAACCCTAT GNGAAATGGA AAGGAAACTA TTCTAAAGCA TAAAAGGTAG AAATATATAT	60
ACCACCCATC AAGAAAGATT ATTTTGNTG AACTCAAGTC ACCAGAGTGG CTAAAGCCCA	120
GTAGAATGGA AATGATTATA TGGAAAGGTGA GGCCAACGGG ACCAGAACAT ACTGTGATAG	180
ACAGNAAGGA GCTGTCTATC TTCTATTCTC CCACAGAAGG AGGTGACTAA GTCANCTGCC	240
CAAGCAATGT TATATCTGCA ATTGATGTNC AGCAGTACAA GTCTGAACAA CTTGGATTGG	300

NTGATTAATG TCCACANTAA ACATACAAGT CNTAATAGCT ATCTCTATAT AGTCTTG	360
TNTTTACAAG GCACTGNCAC ATNATCTCAC CTATTCCTCC	400

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGNATCCAGA ATTGAGTGNA GNGTTCTCTG GNCCACAGTC TCGGTATCTN CTGTGAAATG	60
GGGTATAGAT TCTACAATAA AACAAACACA NNGGCCCTAG GTCAGTGTAA ATGGAGATCA	120
CCANCCACAT TACCACCTCC AACACAGAAT TTTCTTTTC TTAATNCAAT NCGTNTCTTA	180
TAAGTCACTT TNCCCCAACT CACCAATCTA GNTAAGAATT TTTACCCCTGA GAAAAAACAGC	240
TACACTCTAA AATTGCTNCA AAGAAAATGT CTAACATNTG GAAAGAAGGA CTTAACATGT	300
GANGNAGACA CTGGCTCCAT CTAGNGGGTG CTTTNTTTG AAATAATTAT AATNCCNCAT	360
CAAATTTNG GGGGNTACAG CTTATTAGGA ACTTGTATA GAACCAGATT CTGCCACAGA	420
ANCCACGTGG GTTGACAAGT GGTTGNCAGA AGAAAGGTAA TATGGCTTAT NATTAGGGNC	480
TCNCATCTGC AGAGTAATTG	500

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 460 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAATGCTTG ANNCAAATGT CATCTAGTTC CATCTCTACG ACTCTCATGG GGTCCAAAGA	60
AGAGTTTAN TTGAGTTTA GAATGTGAAG TTGTGAAGTG TCTGAAAAC TACATGGTGN	120
TCTGAAAGNC AAACCTTTAG CCTTGGGGGA GAGCATCTAA GACAGNAGGT GAAGGGNAGG	180
GGTTAGAACT AGAGGGATTG AAGAATATTA TCCATATAGG TTAGGGTTAG GTNNNGCAAC	240
GTTTTATAGA ACAAACATTG GCAAGCTACA GCCACAGGCC AGATCTGTCT NCTACCTTCC	300
CACAAAGGTG TAATAACAAA GTTATTACACA AATGTGTGAA TAAACTNNCA TTGGAAAGTG	360
CCCACGCTCC TNGGTTATA CATTGTCTGT GGCTGCTTTC ACACATACAGT AGCACAGGTG	420
AGTGTNTGCA CTGGAGACCA TATGCCCAT AGAGCTTTAA	460

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATCAAGCAAC AGTGTGTTAT GCCTATACTC CATGTTATA TGTGTGTATT	AAAAAATGTA	60
TTTGTATATA TGTGTATGTA TAAGTGTGTG TGTGTGTATG ATGATTCTNC	TCCCGNTTG	120
AAGGTGAAAG AAAGCACACC TTTATTTAAG CATAAACTTT GGGTTTCAGA	TACTGTCTGG	180
AAAAAATGATT TATCTCCCAC TTTGAAATTC CAAAATACGT ACATATATTT	TTTTTTCTT	240
TTCTTTTTA GTTTNAGGGT CTTGCTGTGT TGCCCAGGCT GGAGTGCAGT	AGTGTGATCA	300
TAGNTCACAC AGNCTCTAAC TCCCAGGNTC AAGNTATCTT CCTGCCAG NCTCCTGAGT	360	
AGNTGGGACT		370

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CAAAAAATCA AAGGGAAGNT GGAACCCCTG CCCACCTCTC CATTCCCCAT	TCTGCTGGTG	60
GTGNCTGCTC TTCCTCACAG TACCTCCTGA AAAGTTCAGA ATTCAAGTAA	TACAGAATTAA	120
TTGGGTTGAT TTTCAACGTG TAGTTTAAGA TGAAGAGTTC CGNTTGGTTT	AAACCACTTC	180
ACCTAACCTC TTGGTAACGG TAGTCCTGAG AGTCGCAGT GTCANTGAAA	ATCGTCCTGT	240
GACCACGCGT CAAGCTGCTG ATGGGGGACA GAAACTTCCG GGNCTATCAT	ATCTCCTTGA	300
NCTCGGCCCT CAAATCTGGT AGTTCTGCA CCGAGGGACA CAGTCCACTG	CGATGAAGTA	360
TGTTCAAAAT CGNTTTCTTT AGGGAACTCC TTCCAAAGTC CAATAGTGNA	AGGTGGTCAA	420
GGAAGGATTG GGAAGGAAGN TGNAAAAGTC AGNCGGGAAT CTTGATTGG	NTAGNTGTGG	480
ANANAGGAAA TCACTTGGCC		500

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGAAAGAGGT CTCCTAACAC CCAGACAGTG TAAAAATCCA GTTTTCTTC CTTTGNNNG	60
GAGACAGAGT CTCGCACTGT AGCTCAGGCT GGAGTGCAGT GGCAC	105

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AGTCCCAGCT ACTCAGGAGG CTGGGGCAGG AAGATAGCTT GAGCCTGGGA GTTAGAGGCT	60
GTGTGAGCTA TGATCACACT ACTGCACCTC AGCCTGGCA ACACAGCAAG ACCCTAAAAC	120
TAAAAAAAGAA AAGAAAAAAA AAATATATGT ACGTATTTG GAATTCAAA GTGGGAGATA	180
AATCATTTC CCAGACAGTA TCTGAAACCC AAAGTTTATG CTTAAATAAA GGTGTGCTTT	240
CTTTCACCTT CAAAGCGGGA GAAGAACAT CATAACACACA CACACACTTA TACATACACA	300
TATATACAAA ATACATTTT TAATACACAC ATATAAACAT GGAGTATAGG CATAACACAC	360
TGTTGCTTGA TAAAATATAG GGATCC	386

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TATATTTNAT CAAGCAACAG TGTGTTATGC CTATACTCCA TGTATATATG TGTGTATTAA	60
AAAATGTATT TGTATATATG TGTATGTATA AGTGTGTGTG TGTGTATGAT GATTCTCCTC	120
CCGNTTGAAG GTGAAAGAAA GCACACCTTT ATTTAACAT AAACTTGGG TTTCAGATAAC	180
TGTCTGGAAA AATGATTTAT CTCCCACCTT GAAATTCCAA AATACGTACA TATATTTTT	240
TTTTCTTTTC TTTTTAGTT TNAGGGTCTT GCTGTGTGC CCAGGCTGGA GTGCAGTAGT	300
GTGATCATAG NTCACACAGG CTCTAACTCC CAGGNTCAAG CTATCTCCT GCCCCAGNCT	360
CCTGAGTAGG TGGGACT	377

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTGCAGTAAG CCACGTTCAT GCCACTGTAC TCTAGCGTGG ATGACAGAGA GAGATCCTGT	60
CTTTGGAAGA AAAAAACAAA AAGAAAAAAA AAAGAGTATG GCCATGGCCT TATAATATAG	120
AAGGGGTCAC ATATTAATCT CTGAAAATGG ATCTCTTGTG GGCTTCATA CAAGGCAACA	180
GCCACAGAGT ACGTACCTGA AAGCTGCCTG GGNTTAATGG CTGGNAGTAT GTTCTAACTN	240
GTTCAAGGNAC CCATGTCACN ACTGGTGGTT ACAGAATGTG AATCTCACAC TGTCCNAAAT	300
CGGTTTTATT TTTAAAANGA ATAATTCTAN TACATTACCT TATAAAAAGT AGGTAACCTA	360
ATTTTGGNTT TTAAAAGTGA ATTGAGGGCA GATGCAAGTG GNTCACACCT ATTAATCCCA	420
AATACCTTGG AGAGGGCAAG GTAGGAGGAT TGGTTGGAGC CCAGGAGTCC AAAGACCAGG	480
CTAGGGAATA TTGNAAGAAN GTCCTCTCA CAANAAANAA T	521

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTGCANGAAG CTTTNTTNC TTTTNGGNGG AGACAGAGTC TTGCTGTGTC ANCCCAGGCT	60
GGGGTGCAGT GGNACAGTCA TAGCTCACTG CAACCTTGAA CTCCCTGGNT CATGCGATCC	120
TCCCACCTCA GCCTCTCAAG TAGCTAGAAC TACAGGTGTG CACCACCATG CCTGACTAAC	180
TTGTTTATTN GNGGGAGAGA GAACGNTCTT GCTATATTGC CTAGGCTGGT CNTTGAACTC	240
TTGGCNTNCA AGCAATCCTC CTACCTTGGC CTCTNCAAGG TANTTGGGAT TNATAGGTGT	300
GAGCCACNTG CATCTGGCCT CAATTCACTT TTAAAATNCA AAATTAGGTT ACCTACTTT	360
TATAAGGTAA TGTATTAGAA TTATTCTNN NAAAAATAAA ACCGATTGG GAAAGNGTGA	420
GANTCACATT CTGTAACCAC CAGTGGTGAA ATGGGTCCCC GAACAAGGTA GAACATAACTC	480
CCAGCCATTA ACCCCAGGGA GNGTTCAAGT CCGTNC	516

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGATCCTGTT	TCTTAAAACA	AAAAAAAATT	TACTGATAGN	ACATTGTTCT	AAGTGTATT	60
TTGTATTAAA	TGGATCATT	AATTTAATCT	TCATAACTGA	CATAGGAGTT	GAGTAAC	120
TGTGGTCAA	AA TAGCTAGTAA	GTGATGAGTA	GGCTGGCGC	AGTGGNTCAA	GCCTGTAATC	180
CCAGCACTCT	GGGAGGGCTGA	GGCAGGCAGA	TCACTTGAGG	TCAGGAGTTT	GAGACCAGCC	240
TGGCCAACAT	GGNAAAACCT	CGTCTCTACT	AAAAATACAA	AAATTAGCTG	GGCGTGGTGG	300
GTGCGCACTT	GTAGTCCCAG	CTACTCGGAA	GGGTTGAGGC	AGGAGGAATC	GCTTGGTCCC	360
CGGGAGGGAG	AGGTTGNTNG	TGNAGCTGAG	ATCACGCCAC	TNGCACTCCA	GGCTGGNAA	420
CAAAAGGGAG	ACCTTNCTC	AAAAAAAAT	NAAAATAAAA	AGTGATGAGT	AGGATTGGGA	480
CCCNAGACAT	CTTTCTCCA	AGACC				505

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTGCAGNCTC	AAACCCTTGT	CCTGGGATCA	AACAATCCTC	CCACCTCAGC	CTTCAAAGTA	60
GATAGAACTA	CAGGCATGCA	CTACCATGCC	TAATTTTTA	AAAAAAAATT	TTTTTCAGA	120
GATGAGATCT	CACTGTGTTT	CCCAGGNTTG	TCCGGAACTC	CTGGACTCAA	GCGATCCTCC	180
CACCTTGGGC	TGCCAAAGTG	TTGGGATTAC	AGGCATGAGC	CACCATGCCT	GGCCATACAC	240
TTTTTTTTT	TTTTAANCA	AGACGGAGTC	TNGTTCTGTC	GCCCAGACTG	GAGTGCAGGG	300
GCGTNNATCT	TGGCTCACTT	GAAAGCTTCG	CCTCCCAGGG	TTCATGCCGT	TCTCCTGNCT	360
CAGCCTCCCA	AGTNGGTGGG	ACTACAGGNA	TCTGCACCAC	GNCCGGTTAT	TTNTTGGGTT	420
TGNNGNAGGG	ACGGGGTTTC	ACCATGTTAG	GCAGGATGAC	TTCGGACTTC	CNGACCCAAG	480
ATCACCCCTGC	TCGGCTCCCA					500

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 440 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAATTCCAGA CGAGCCTGGG CAACACAGTG AGACTCTATC ACTACAAAAA AATTTAAAAA	60
TTAGCTAAAG TTGATGGNAC ATGCCTGCAG TCCCAGCTAC TCAGGAGGCT GGGGCAGGAA	120
GATAGCTTGA GCCTGGGAGT TAGAGGCTGT GTGAGCTATG ATCACACTAC TGCACCTCAG	180
CCTGGGCAAC ACAGCAAGAC CCTAAAACTA AAAAAGAAAA GAAAAAAAATATATGTAC	240
GTNTTTGGGG AATTCAAAG TGGGAGATAA ATCATTTC CAGACAGTNT CTTGAAACCC	300
AAAGTTTATG CTTAAATAAA GGTGTGCTTT CTTTCACCTT CAAANGCGGG AGAAGGATCA	360
TCATNCACAC ACACACACTN ATCATNCACA TTTTACAAA TNCAATTNNN NAATACAACA	420
CATTTAACCA TGGGGTTTG	440

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGATCCTGTT TCTTAAAACA GAAAAAAATT TACTGATAGN ACATTGTTCT AAGTGTATTA	60
TTGTATTAAA TGGATCATTT AATTAACTCT TCATAACTGA CATAGGAGTT GAGTAACCTG	120
TGTGGTCAAA TAGCTAGTAA GTGATGAGTA GGCTGGCGC AGTGGCTCAA GCCTGTAATC	180
CCAGCACTCT GGGAGGCTGA GGCAGGCAGA TCACTTGAGG TCAGGAGTTT GAGACCAGCC	240
TGGCCAACAT GGNAAAACCT CGTCTCTACT AAAAATACAA AAATTAGCTG GGC GTGGTGG	300
NTGCGCACTT GTAGTCCCAG CTACTCGGAA GGCTNGAGGC AGGAGGAATC GCTTGATCCC	360
NGGGAGGGAG AGGTTGGTNG TGANGCTGAG ATCACGNAC TTGNACTCCA GNCTGGNAA	420
CAAANGNGAG ATCTTNTCTC AAAAAAAAAT AAAANTAAAA NGTGATGAGT AGGATTTGGA	480
CCCCAGACAT CCTNTCTCCA GGACCTGGNA TTC	513

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAATTCTGG NCTCAAGTGA TCCTCTCACC TCAGCCTCCC AAATTGCTGG GATTAGAGTG	60
TGAGCCACTG TGCCTAGCCT GCATATATCT ATTTTTAATG ACTGCTAAAT CTCATTGTAT	120
GAAAATTAT GTCCTAGCTA TAAAATTGAG TAGCACATGT TTAATTTCAG	180
ATGTTTAAA CTAATATTTC CCAAAGTATA GTATGGCATT TTAGGTATGA TATGATCTT	240
NNTCCTCTTC GTACTCATT TTATAGTTAT GGCCTGTGCA ACTGGTTCC CATTATATG	300
AATGATACAG AGCTTCCTAT TAAGAAAAAG TTCAGCTTGG GGAAAAAAAAGTGAATTGT	360
CAACTTNGAG GGAAAAAAAGT GAATTATTGG	390

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TCAAGTACCT CCCTGAATGG ACTGCGTGGC TCATCTTGGC TGTGATTCA GTATATGGTA	60
AAACCCAAGA CTGATAATTG GTTTGTCACA GGAATGCCCG ACTGGAGTGT TTTCTTCCT	120
CATCTCTTA TCTTGATTAA GAGAAAATGG TAACGTGTAC ATCCCATAAC TCTTCAGTAA	180
ATCATTAAATT AGCTATAGTA ACTTTTCAT TTGAAGATTG CGGCTGGGCA TGGTAGCTCA	240
TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCAGGGCAG ATCACCTAAC CCCAGAGTTC	300
AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA GAAAATACAA AAATTNGNCG	360
GGNATG	366

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AACACCAGGG NCATGAGGGC ACTAATCATA ATGAGATATG CCTGCTGGAG TCGAAGTGGA	60
CCTTTCCAGT GAATGGAAAT CATTCCCACC ACACCAAAAT TCCAGATCAG GAGTGNAACA	120
GTAATGTAGT CCACAGCAAC GTTATAGGTT TTAAACACTT CCCTGAAAAAA AAATTACACA	180
GATTTAAAAA GATGTACAAT AATTCCACC AAAACATTAT TTAGAATAAT GTGATGGCTC	240
CCAAACATTA GATATTAATN TCCCACCTTT ATAATTTCAG CATAACCTAT ATCAACTGTG	300

CTATTATTTA TTTAATNCTT CCCTNTAAAT TAATTTACTC TTTTTTGTT TTTGTTTTG	360
NGTTTGGAGC CAGTGTCTCA TTTTGGTTGC CCAGGCTTGG AGTAAAGTGG GTGCAATCAC	420
GGCTCAACTG NAGTCTTNC CTCCNGGAGA TCAGGTNGGT CTTCCCCAGG TCCAANCTCC	480
TAAGTTGGTT NGGANAAC	498

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 469 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAAACAACAG GGNCATGAGG GCACTAATCA TAATGAGATA TGCCTGCTGG AGTCGAAGTG	60
GACCTTCCA GTGAATGGAA ATCATTCCA CCACACAAA ATTCCAGATC AGGAGTGAAA	120
CAGTAATGTA GTCCACAGCA ACGTTATAGG TTTAAACAC TTCCCTGAAA AAAAATTACA	180
CAGATTTAA AAGATGTACA ATAATTCCA CCAAAACATT ATTTAGAATA ATGTGATGGC	240
TCCCAACAT TAGATATTAA TNTCCACCT TTATAATTTC ACCATAACCT ATATCAACTG	300
TGCTATTATT TATTAATNC TTCCCTCTAA ATTAATTAC TCTTTTTTG TTTTGTGTTT	360
TGTGTTTGGA GCCAGTGTCT CATTGGTT GCCCAGGCTT GGAGTAAAGT GGGTGCAATC	420
ACGGCTAAC TGNAGTCTT ACCTCCGGA GATCANGTTG GTCTTCCC	469

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTTTATCAAG TACCTCCCTG AATGGACTGN GTGGCTCATC TTGGCTGTGA TTTCAGTATA	60
TGGTAAAACC CAAGACTGAT AATTGTTTG TCACAGGAAT GCCCCACTGG AGTGTGTTCT	120
TTCCCTCATCT CTTTATCTTG ATTTAGAGAA AATGGTAACG TGTACATCCC ATAACCTCTC	180
AGTAAATCAT TAATTAGCTA TAGTAACCTT TTCATTTGAA GATTCGGCT GGGCATGGTA	240
GCTCATGCCT GTAATCTTAG CACTTTGGGA GGCTGAGGCG GGCAGATCAC CTAAGCCCAG	300
AGTTCAAGAC CAGCCTGGGC AACATGGCAA AACCTCGTAT CTACAGAAAA TACAAAAATT	360

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTCACTGGTGT	TGGCGGGGAG	TGTCTTTAG	CATGCTAATG	TATTATAATT	AGCGTATAGT	60
GAGCAGTGAG	GATAACCAGA	GGTCACTCTC	CTCACCATCT	TGGTTTGGT	GGGTTTTGGC	120
CAGCTTCTTT	ATTGCAACCA	GTTTTATCAG	CAAGATCTT	ATGAGCTGTA	TCTTGTGCTG	180
ACTTCCTATC	TCATCCCGNA	ACTAAGAGTA	CCTAACCTCC	TGAAATTGA	AGNCCAGNAG	240
GTCTTGGCCT	TATTNACCC	AGCCCCTATT	CAAAATAGAG	TNGTTCTTGG	NCCAAACGCC	300
CCTGACACAA	GGATT					316

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTGCAGNCCG	GGGGATCCTG	GTAAAAGTCA	CAAGGTCAGC	CTACTAAAGC	AGGGAAAAGT	60
AAAGGCAAGT	AAACACGTGC	AGACAAAAAA	AGGGATAAAAG	AAAAGGAATT	AAGAAACTAG	120
CATTTTAAN	GTGGGGGAGG	TGAATGCTTC	CCAGAAATGGG	TTTATATCAC	TTGCTTGNNG	180
GCCTTCTGAG	TGTTGGNAAC	AACCTGTCAT	CATCACACAT	ACCTGTCATC	TTAATGGTC	240
TCCATACATT	ACTAATAGAT	TATACAGATG	GCCATCACTT	AACACTTCCA	CTCACTCAAT	300
TTGTNCAACA	TGCAAGGTTA	CCCTTTTT	TNGCTTACNG	CCACAAAGCA	TTGGANAAGG	360
TTTGTGATT	TTACTAGCCN	CCACTTCATC	AAATTAAAGC	ATTTCTTT	TCCTNTTAAC	420
ANCCAGGACA	GGNTTNAACN	AAGGAAAT				448

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTGCAGCTCC AAGCACCTT TTCAAATTCA GCTTCTGTG ATTCAGACC ACATATGCAA	60
GGAACATATCT TACCTTAATT AATAAGACTT TAAAATCCTT GTGTCAGAGG CGTTTGGACC	120
AGAGCAACTC TATCTTGAAT AGGGGCTGGG TAAAATAAGG CCAAGACCTA CTGGGCTGCA	180
TTTGCAGGAG GTTAGGTACT CTTAGTTACG GGATGAGATA GGAAGTCAGC ACAAGATACA	240
GCTCATAAAG GATCTTGCTG ATAAAACCTGG TTGCAATAAA GAAGCTGGNC AAAACCCACC	300
AAAACCAAGA TGGTGAGGAG AGTGACCTCT GGTTATCCTC ACTGNTCACT ATACGNTAAT	360
TATTATACAT TAGCATGCTA AAAGACACTC CCCGCAACAA CCATGANAGG TTTACAAGTT	420
NCCATGGNAA CGNNCCCGGA NGNTANCTTG	450

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 388 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTGNAGCCTC CACCACCCAG GTTCAGGTGA TTCTCCTGCC GTAGNCTCAT GAGTAGNTGG	60
GATTACAGGC ATGTGCCACC ATGCCCGACT AATTTTATA TTTTTAGTAG AGACGGGGTT	120
TCACCATGTT GGGCAGGCTG GTCTCAAACCT CCTGACCTCA AGTGATCTGC CCACCTTGGC	180
CTCCCAAAGT GCTGGGATTT CAGGCGCCTG GCCTGTTACT TGATTATATG CTAAACAAGG	240
GGTGGATTAT TCATGAGTTT TCTGGAAAG AGGTGGCAA TTCCCGAAC TGAGGGATCC	300
CTCCCCTTNN NAGACCATAAC AAGGTAACCTT CGGGACGTTG GCATGGNATC TTGTTAAACT	360
TGTCATGGNG TTGGGGGGGA GTGTCTTT	388

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTGCAGAAAGT ATGTTTCCTG TATGGTATTA CTGGATAGGG CTGAAGTTAT GCTGAATTGA	60
ACACATAAAAT TCTTTCCAC CTCAGGGNCA TTGGGCGCCC ATTGCTCTTC TGCCTAGAAT	120

ATTCTTCCT TTTCTAACCT TGGTGGATTA AATTCCGTGTC ATCCCCCTCC TCTTGGTGT	180
ATATATAAAG TNTTGGTGCC GCAAAAGAAG TAGCACTCGA ATATAAAATT TTCCTTTAA	240
TTCTCAGCAA GGNAAGTTAC TTCTATATAG AAGGGTGCAC CCNTACAGAT GGAACAATGG	300
CAAGCGCACA TTTGGGACAA GGGAGGGAA AGGGTTCTTA TCCCTGACAC ACGTGGTCCC	360
NGCTGNTGTG TNCTNCCCCC ACTGANTAGG GTTAGACTGG ACAGGCTAA ACTAATTCCA	420
ATTGGNTAAT TTAAAGAGAA TNATGGGGTG AATGCTTGG GAGGAGTCAA GGAAGAGNAG	480
GTAGNAGGTA ACTTGAATGA	500

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTGCAGAGTA ATTGCAACTG GAGTTGTCTT AAGATAATGT CACATATCCA TCTTCCCCTT	60
GTTTCTCATT CACAGAAAAA CATTTTATT CCAGGTGCCA ATATTCCAG CCAAAAAGAC	120
TTTACTTCTG ACTCCCTTAT ATTTAGGATG GCTATGAGAA CAAGTAAGGG CAATGACTTC	180
TAGGGAGATG TGTTGTGTAT GGAACTTCTA AGGAGAGAAT TCTGCTGACA TGTCCTATGT	240
TCTTTCTCC CCTACTCCTT CCTACTGTCA GAAATGAAGG CTAGGGCTCC AGCCTGGACC	300
CTGAAGTAAG CTAGAGGTTA GAAGCTAAAG AAGAAAGAAG GAGATTGAGT CCTTGGATGA	360
ACGTGAAGCC ACCCTACTAA TCTGGACTGN CTACCTCTGN ACTACTCTAT GAGAGAGAAA	420
GTATGTGCAT TATTT	435

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 439 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CATGCTCTT GTCCCTGTGA CTCTCTGCAT GGTGGTGGTC GTGGNTACCA TTAAGTCAGT	60
CAGCTTTAT ACCCGGAAGG ATGGGCAGCT GTACGTATGA GTTTGGTTTT ATTATTCTCA	120
AAGCCAGTGT GGCTTTCTT TACAGCATGT CATCATCACC TTGAAGGCCT CTGCATTGAA	180
GGGGCATGAC TTAGCTGGAG AGCCCACCT CTGTGATGGT CAGGAGCAGT TGAGAGAGCG	240

AGGGGTTATT ACTTCATGTT TTAAGTGGAG AAAAGGAACA CTGCAGAAGT ATGTTTCCTG	300
TATGGTATTA CTGGATAGGG CTGAAGTTAT GCTGAATTGA ACACATAAAAT TCTTTCCAC	360
CTCAGGGGCA TTGGCGCCC ATTGNTCTTC TGCCTAGAAT ATTCTTCCT TTNCTNACTT	420
GGGNGGATTA AATTCCGT	439

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TCCATCTCTA CGACTCTCAT GGGGTCCAAA GAAGAGTTT AATTGAGTTT TAGAATGTGN	60
AGTTGTGAAG TGTCTGAAAA ACTACATGGT GNTCTGAAAG NCCTACTTT AGCCTTGGGG	120
GAGAGCATCT AAGACAGNAG GTGAAGGGGA GGGGTTAGAN CTAGAGGGAT TGAAGAATAT	180
TATCCATATA GGTTAGGGTT AGGTGTGGCA ACGTTTATA GAACAAACAT TGGNAAGCTA	240
CAGACACAGG CCAGNTCTGT CTNCTACCTN TCCACAAAGG TGTNATAACA AAGTTANNCA	300
CAAATGTGTG AATAAACT	318

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTTGCAAAGT CATGGATTCC TTTAGGTAGC TACATTATCA ACCTTTTG AATAAAATG	60
AATTGAGAGT GTTACAGTCT AATTCTATAT CACATGTAAC TTTTATTG ATATATCAGT	120
AATAGTGCTT TTTCNTTTT TTTTTTTNTT TTTTTNNNTT TTNGGGANA GAGTCTCGCT	180
CTGTCGCCAG GTTGGAGTGC AATGGTGCAG TCTGGCTCA CTGAAAGCTC CACCNCCGG	240
GTTCAAGTGA TTCTCCTGCC TCAGCCNCCC AAGTAGNTGG GACTACAGGG GTGCGCCACC	300
ACGCCTGGGA TAATTTGGG NTTTTAGTA GAGATGGCGT TTCACCACNT TGGNGCAGGC	360
TGGTCTTGGGA ACTCCTGANA TCATGATCTG CCTGCCTTAG CCTCCCCAAA GTGCTGGGAT	420
TNCAGGGGTG AGCCACTGTT CCTGGGCCTC	450

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CTGCAGNTGA	GCCGTGATTG	CANCCACTTT	ACTCCNAGCC	TGGGCAANCA	AAATGAGACA	60
CTGGCTNCAA	ACACAAAAAC	AAAAACAAAAA	AAAGAGTAAA	TTAATTAAA	GGGAAGTATT	120
AAATAAATAA	TAGCACAGTT	GATATAGGTT	ATGGTAAAAT	TATAAAGGTG	GGATATTAAT	180
ATCTAATGTT	TGGGAGCCAT	CACATTATTC	TAAATAATGT	TTTGGTGGAA	ATTATTGTAC	240
ATCTTTAAA	ATCTGTGTA	TTTTTTTCA	GGGAAGTGT	TAAAACCTAT	AACGTTGCTG	300
TGGACTACAT	TACTGTTGCA	CTCCTGATCT	GGAATTGG	TGTGGTGGGA	ATGATTTCCA	360
TTCACTGGAA	AGGTCCACTT	CGACTCCAGC	AGGCATATCT	CATTATGATT	AGTGCCCTCA	420
TGGCCCTGGT	GTTTATCAAG	TACCNCCTG	AATGGACTGG	GTGGCTCATC	TTGGCTGTGA	480
TTTCAGTAT						489

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CTGCAGNCTT	GACCTCCTGG	GATCAATCGA	TCCTCCCACC	TCAGCCTCCT	AAGTAGCTGG	60
AACTACAGGT	GTGCACCACC	ATGCCCGGCT	AATTTTGTA	TTTCTGTAG	ATACGAGGTT	120
TTGCCATGTT	GCCCAGGCTG	GTCTTGAAC	CTGGGCTTAG	GTGATCTGCC	CGCCTCAGCC	180
TCCCAAAGTG	CTAAGATTAC	AGGCATGAGC	TACCATGCC	AGCCGAAATC	TTCAAATGAA	240
AAAGTTACTA	TAGCTAATTA	ATGATTTACT	GAAGAGTTAT	GGGATGTACA	CGTTACCATT	300
TTCTCTAAAT	CAAGATAAAG	AGATGAGGAA	AGAAAACACT	CCAGTGGGC	ATTCCCTGTGA	360
CAAACAAATT	ATCAGTCTTG	GGTTTACNA	TATACTGAAA	TCACAGCCAA	GATGAGCCAC	420
GCAGTCCATT	CAGGGAGGTA	CTTGATAAA				449

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTCTTGCCGT	TCCCGACCCG	AGCCTGGTGC	CCCTTCCCCA	TTATGATCCT	TNTCGCTTCC	60
GGCGGCATCG	GGATGCCCG	CGTTGCAGGC	CATNCTGTCC	CAGNCAGGTA	GATGACGACC	120
ATCAGGGACA	GCTTCAAGGA	TCGCTCGCGG	CTCTTACCAAG	CCTAACTTCG	ATCATTGGAC	180
CGCTGATCGT	CACGGCGATT	TATCCCGCCT	CGGCGAGCAC	ATGGAACGGG	TTGGCATGGA	240
TTGTAGGCCGC	CGCCCTATAC	CTTGTCTGCC	TCCCCCGCGT	TGCGTCGCGG	TGCATGGAGC	300
CGGNCCACCT	CGACCTGAAT	GGAANCCGGC	GGCACCTCGC	TAACGGATTTC	ACCACTCCAA	360
GAATTGGAGC	CAATCAATTC	TTGCGGAGAA	CTGTGAATGC	NCAAACCAAC	CCTTGGCAGA	420
ACATATCCAT	CGCGTCCGCC	ATCTCCANCA	GCCGCACGCG	GCGCATCTCG	GGCAGCGTTG	480
GGTCCTGCAG						490

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGCAGTGT	TAAAAAATAA	AATAAACTAA	AAGTTTATTT	ATGAGGAGTA	CACTGCTTTC	60
TTGTAAACAC	ATGTACAAGC	CATATAATAG	AGTTCATTTTC	NNACCCTAGT	TACGGAAACA	120
CTAGAAAGTC	TNCACCCGGC	CAAGATAACA	CATCTTCTAGG	TAAAAATAGC	AAGAAATATT	180
TTATGGTTG	TTTACTTAAA	TCATAGTTTT	CAGGTTGGGC	ACAGTGGNTC	ATGCCTGTAA	240
TCCCAGCACT	TTATGCGGCT	GAGGCAGGCA	GATCAGTTGA	GGTCAGAAGT	TTGAGACCAG	300
CCTGGGCAAT	GTGGCAAAAC	CTCATCTCCA	CTAAAAATAC	AAAAATTAGC	CAGGCATGGT	360
GGTGCACACA	TGTTAATTCC	CAGCTACTTG	GGAGGNTTGA	GACAGGAGGG	TCGCTTGGNC	420
CTAGGAGGGA	AGAAGTTGNA	GGGANCTTAA	TGTCACTGCA	CTCTAGNTTG		470

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CACTCAATTC	TGAATGCTGC	CATCATGATC	AGTGTCAATTG	TTGTCATGAC	TANNCTCCTG	60
GTGGTTCTGT	ATAAATACAG	GTGCTATAAG	GTGAGCATGA	GACACAGATC	TTTGNTTTCC	120
ACCCCTGTTCT	TCTTATGGTT	GGGTATTCTT	GTCACAGTAA	CTTAACGTAT	CTAGGAAAGA	180
AAAAATGTTT	TGTCTTCTAG	AGATAAGTTA	ATTTTAGTT	TTCTTCCTCC	TCACTGTGGA	240
ACATTCAAAA	AATACAAAAAA	GGAAGCCAGG	TGCATGTGTA	ATGCCAGGCT	CAGAGGCTGA	300
GGCAGGAGGA	TCGCTTGGGC	CCAGGAGTTC	ACAAGCAGCT	TGGGCAACGT	AGCAAGACCC	360
TGCCCTCTATT	AAAGAAAACA	AAAAACAAAT	ATTGGAAGTA	TTTTATATGC	ATGGAATCTA	420
TATGTCATGA	AAAAATTAGT	GTAAA				445

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CCTGTATTAA	TACTGAACCA	CCAGGAGGAT	AGTCATGACT	ACAATGACNC	TGATCATGAT	60
GGCAGCATTG	AGAATTGAGT	GCAGGGCTCT	CTGGCCCACA	GTCTCGGTAT	CTTCTGTGAA	120
TGGGGTATAG	ATTCTACAAT	AAAACAAACA	CAAAAGCCCT	AGGTCAGTGT	TAATGGAGAT	180
CACCAACCAC	ATTACCACCT	CCAACACAGA	ATTTCTTTT	TCTTAATTCA	ATTGNATCT	240
TATAAGTCAC	TTTCCCCAA	CTCACCAATN	CTAGCTAAGA	ATTTTAACC	TGAGAAAAAC	300
AGCTACACTC	TAAAATTGCT	TCAAAGAAAA	TGTCTAACAT	ATGGAAAGAA	GGACTTAACA	360
TGTGAAGCAG	ACACTGGCTC	CATCTAGTGG	GTGCTTTATA	TTGAAATAAT	TATAATACCT	420
CATCAAATT	TTTNGGGTAC	AGNTTATTAG	GAACCTGGTA	TGGAACCAGA	TTCTGCCACA	480
GAAACCACGN	GGGCTG					496

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CATTAGATAA TGGNTCAGGG TGGCCAAGGC TCCGTCTGTC GTTGTGCTCC TGCCGTTCTC	60
TATTGTCATT CTATAAGCAC AAGAAAAACA TTTTCAGTAA ATCAGATTCT CAGCAGAAC	120
AAGGTAACGG TTAGACCTGG GATTAACAAAC AGACCCGTCA CTATGAGTTC TAAAAAACCTG	180
AAGCAAGAAA AAACAATGTA CAGGAAGTAT GCAGTTAAA AGTCTAGATT ATCTATCATT	240
GTTCACTGAA GGCATTCAGG TCCTCTCTT TACCTGGTC TTGGNTTGCT CCATTCTCTC	300
TGTTCATCCC AACATACACA ATTGTACTTA TCCTTGAGA TGTACCTTAA ATACTGACAC	360
CTGCATGAAA ACTTGTTAC TGGCTGCAGG TCCAAGCACC TTTTCNAAA TTCAGCTTTC	420
TGTGATTCA GACCACATAT GCAAGGAAC ATCTTACCTT AATTAATAAG ANTTTAAAT	480
CCTTGTGTCA GAGGCG	496

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AGGANCGCTT GGGCCCAGGA GTTCACAAGC AGCTTGGCA ACGTAGCAAG ACCCTGCC	60
TATTAAAGAA AACAAAAAAC AAATATTGGA AGTATTTAT ATGCATGGAA TCTATATGTC	120
ATGAAAAAAAT TAGTGTAAA TATATATATT ATGATTAGNT ATCAAGATT AGTGATAATT	180
TATGTTATNN NGGGATTCA ATGCCTTTT AGGCCATTGT CTCAAAAAAT AAAAGCAGAA	240
AACAAAAAAA GTTGTAACTG AAAAATAAAC ATTTCCATAT AATAGCACAA TCTAAGTGGG	300
TTTTGNTTG TTTGTTGNT TGTTGAAGCA GGGCCTTGCC CTNCCACCCA GGNTGGAGTG	360
AAGTGCAG	368

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAATTCCATT TTTTTTTTTT TTTTTTTTT TTNCTCCTAA TGTTTTATT GTNCCTTAGA	60
TAACTGGATA GNACAAAGTT NGNCTTNGTT TTTTACTTAA AAAACGTACT TTCCGCATAC	120

TGTNGCCCGT ATGACTTTCC TGTCCCATCG GAAACCAGAG TTTCCCCAGG TGAGCCCTTC	180
CTATCTGNGG NTACATGATT TAGCTAATTT ACAAGAAGA GAGTAATTCC TTNGGATTAT	240
TATCAACATG AAACCTGGAC TATGTCTCTA TAAGGGTGAA CACTGATTT TTTTTCTTT	300
TTAGAAACAA AAACCATCCA CTTATTAATC CAAACTACGG GATTGGATT ACAACAATCA	360
TCGCATNAAC TGAACATACG AAGTTACAC TCAAGGGAAT NACAGAAGAA CGTTGNACAA	420
TNTNTCTTAC GGGGTACGNG AATTCAAACA ATGTGGGGAN AGGAACATTCA NTCTACAAAN	480
TCTGACCATC GNTTCAGTAT	500

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GAATTCCATT ACTCTTCTTT AATTCTACCG TCTTGGGCA TACATCTCAT TTGNTGTGGA	60
AGAAGGTCTG ACAGNAGGGC TGACAGCACC GATTCTAAC ACATTCTTT CATCATACAA	120
AGAGTAAGAC CCTAGAATAA TGGGACCATC TGCTACCACG ACAGAGCTGC CTTACTGGCT	180
GTAGAAAAAG ACTGCTTGTG TGGGAGAGAA GAATGAGGAC AGAGGAGGCA TCTGGGCAA	240
GTGAGCGTAC AAGTATNTCT ACAAAATTCAAG AATTGGTGG AAAATCCAAA TTTGNCTTCA	300
ACATGATAGA GAATTGATGA GAAAATAGCT GTNCTGTTTC CAAAATTAC TGAATTGGG	360
AACCTGAGGT TAAAACCTTT AGGATNAAGC AACTCAGGTT CAAGACTTNG NCTNGGGAAAG	420
GAATGGAAAC ACAGACGGGA ATGAGTNCA	450

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAACTGTATT TATACAGNAA CCACCAGGAG GATAGTCATG ACAACAATGA CAAACTAGGA	60
ATAGCCCCCT TTCACTTCTG AGTCCCAGAG GTTACCCAAG GCACCCCTCT GACATCCGGC	120
CTGCTTCTTC TCACATGANA AAAACTAGCC CCCAGTNTGA TCCGCAGGTN GAGGAATNCC	180

CCGGGTCGAG GTTCGGATCC TGGATGACAG ACCCTCTCGC CCCTGAAGGN GATAACCAGGG	240
TGTGGTACAT GGACGGNTAT CACAACAACC GCTTCGNACG TGAGTACAAG TCCATGGTTG	300
ACTTCATGAA CACGGACAAT TTCACCTCCC ACCGTCTCCC CCACCCCTGG TCGGGCACGG	360
GGNAGGTGGT CTNCAACGGT TCTTTCTNCT TCAACAAAGTT CCAGAGCCAC ATCATCATCA	420
GGTTTGGACC TGAAGANAGA GAACATCCTC	450

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGATCCCTCC CCTTTTTAGA CCATACAAGG TAACTTCCGG ACGTTGCCAT GGCATCTGTA	60
AACTGTCATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA	120
TAGTGAGCAG TGAGGATAAC CAGAGGTCAC TCTCCTCACC ATCTTGGTTT TGGTGGGTTT	180
TGGCCAGCTT CTTTATTGCA ACCAGTTTA TCAGCAAGAT CTTTATGAGC TGTATCTTGT	240
GCTGACTTCC TATCTCATCC CGTAACTAAC AGTACCTAAC CTCCTGAAA TNGCAGCCCA	300
GTAGGTCTTG GNCTTATTTC ACCCAGCCCC TATTCAAGAT AGAGTTGCTC NTGGTCCAAA	360
CGCCTCTGAC ACAAGGATT TAAAGTCTTA TTAATTAAGG TAAGATAGGT CCTTGGATAT	420
GTGGTCTGAA ATCACAGAAA GCTGAATTG GAAAAAGGTG CTTGGAGCTG CAGCCAGTAA	480
ACAAGTTTC ATGCAGGTGT	500

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTGCAGTGAG CCAAAATCGT GCCACTGCAC TTCACTCCAG CCTGGGTGAC AGGGCAAGGC	60
CCTGCTTCAA CAAACAAACA AACAAACAAA AACCCACTTA GATTGTGCTA TTATATGGAA	120
ATGTTTATTTC TTCAGTTACA ACTTTTTTG TTTCTGCTT TTATTTGTTG AGACAATGGC	180
CTAAAAAGGC ATTGAAATNC CAAAATAACA TAAATTATCA CTAAATCTTG ATAACATAATC	240
ATAATATATA TATTTTACAC TAATTTTTC ATGACATATA GATTCCATGC ATATAAAATA	300
CTTCCAATAT TTGTTTTTG TTTCTTTAA TAGAGGCAGG GTCTTGCTAC GTTGCCCAAG	360

CTGCTTGTGA ACTCCTGGC CCAAGCGATC CTCCTGCCTC AGCCTCTGAG CCTGGCATT	420
CACATGCACC TGGCTTCCTT TTTGTNTTT TTGAATGTTC CACAGTGAGG AGGAAGAAAA	480
CTNAAAATTA ACTTATCTCT	500

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTGCAGATGA GAGGCACTAA TTATAAGCCA TATTACCTTT CTTCTGACAA CCACCTGTCA	60
GCCCCACGTGG TTTCTGTGGC AGAATCTGGT TCTATAACAA GTTCCTAATA AGCTGTAGCC	120
AAAAAAATTT GATGAGGTAT TATAATTATT TCAATATAAA GCACCCACTA GATGGAGCCA	180
GTGTCTGCTT CACATGTTAA GTCCTTCTT CCATATGTTA GACATTTCT TTGAAGCAAT	240
TTTAGAGTGT AGCTGTTTT CTCAGGTTAA AAATTCTTAG CTAGGATTGG TGAGTTGGGG	300
AAAAGTGACT TATAAGATAC GAATTGAATT AAGAAAAAGA AAATTCTGTG TTGGAGGTGG	360
TAATGTGGGT GGTGATCTTC ATTAACACTG ANCTAGGGNT TTGGGGTTTG GTTTATTGTA	420
GAATCTATAC CCCATTCA NA GAAGATACCG	450

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTGCAGCCAG TAAACAAGTT TTCATGCAGG TGTCAGTATT TAAGGTACAT CTCAAAGGAT	60
AAGTACAATT GTGTATGTTG GGATGAACAG AGAGAATGGA GCAAGCCAAG ACCCAGGTA	120
AAGAGAGGAC CTGAATGCCT TCAGTGAACA ATGATAGATA ATCTAGACTT TTAAACTGCA	180
TACTTCCTGT ACATTGTTT TTCTTGCTTC AGGTTTTAG AACTCATAGT GACGGGTCTG	240
TTGTTAATCC CAGGTCTAAC CGTTACCTTG ATTCTGCTGA GAATCTGATT TACTGAAAAT	300
GTTTTTCTTG TGCTTATAGA ATGACAATAG AGAACGGCAG GAGCACAACG ACAGACGGAG	360
CCTTGGCCAC CCTGAGCCAT TATCTAATGG ACGACCCAGG GTAACCTCCG GCAGGTGGTG	420
GAGCAAGATG AGGAAGAAGA TGAGGAGCTG ACATTGAAAT ATGGCGGCNA GCATGTGATC	480

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTGCAGTGTT CCTTTCTCC ACTTAAAACA TGAAGTAATA ACCCCTCGNT CTCTCAACTG	60
CTCCTGACCA TCACAGAGGA TGGGCTCTCC AGCTAAGTCA TGCCCCTTCA ATGNAGAGGC	120
CTTCAAGGTG ATGATGACAT GCTGTAAAGA AAAGCCACAC TGGGTTTGAG AATAATAAAA	180
CAAAACTCAT ACGTACAGCT GCCCATCCTT CCGGGTATAA AAGCTGACTG ACTTAATGGT	240
AGCCACGACC ACCACCATGC AGAGAGTCAC AGGGACAAAG AGCATGATCA CATGCTTGGC	300
GNCATATTTC AATGTCAGNT CCTCATCTTC TTCCATCATCT TGNTCCACCA CCTGCCGGGA	360
GTTACCNNTGG GTCGTCCATT AGATAATGGG TCAGGGTGGC CAAGGCTCCG TCTGTCGTTG	420
TGCTCCTGCC GTTCTCTATT GTCATTCTAT AAGCACAAGA AAAACATTTN CAGTAAATCA	480
GATNCTCAGC AGAATCAAG	499

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TAACTCCCAG GNTCAAGATN TCTNCCTGCG TTAGCCTCCT GAGTAGCTGG GACTATAGGT	60
ATGTGCCACT ATTCCCTGAAA ACATAATCAG TTTTGAAGGT AGTGTCTGGG CTGGGCGCAG	120
TGGNTCACGC CTTCAATCCC AGCACTTGG GAGGNCGAGG TGGGCGGATC ACCTGAGGTC	180
AGGAGTTCGA GACCAGCCTG ACCAACATGG GATAAGACTC CATCTCTACT AAAAATACAA	240
AAAATTAGCC AGGCATGGTG GNGCATGCCCT GTAATCCCAG CTACTCAGGA GGNTGAGGNA	300
GGAGAATTGG TTGGAACCTA GGAAGCAGAG GCTGTGGTGG AGCCGAGATC GCACCATTGG	360
ACTCCAGGCT GGGNAACAAG AGTAAAATC CNTCTTAAAA AAAAAAAA AAAGGTAGNG	420
TTTTGNCCGG NGCGGGGGGT CACGCCTGTA ATCCCAGNAT TGGGGANGGC AAGGNGGGGG	480
GTCANNANGN NAGNAGTCCG	500

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAATTCTGCT	GACATGTCCT	ATGTTCTTT	CTCCCCTACT	CCTTCCTACT	GTCAGNAATG	60
AAGGGTAGGG	CTCCAGCCTG	GACCCTGAAG	TAAGCTAGAG	GTTAGAAGCT	AAAGAAGAAA	120
GAAGGAGATT	GAGTCCTTNG	ATGAACGTGA	AGCCACCGTA	CTAATCTGGA	CTGCCTACCT	180
CTGCACTACT	CTATGAGAGA	GAAAGTATGT	GCATTATTTA	AACCAGTTGG	GTTGATTTTC	240
TATTAACAAA	GTCAGAAACA	TCTCTGTAAA	AAGCCAGACT	GAATATTTA	AGCTCTATGG	300
GTCATATGGT	CTCCAGGGCA	AACACTCAAC	TGTGCTACTG	TAGTGTGAAA	GCAGGCACAG	360
ACAATGTATT	AACCAAGGAG	GGTGGTCACT	TTCCAATGAA	AGTTTATCAC	AAATTGGNNGA	420
ATACTTGGTA	TTACACCNNNG	GGGGAAGGTA	GGAGAAGATC	TTGCCTGTGG	TTGTNGNTGG	480
CAATGTTGGT	CTTTTATACG	NG				502

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAATTCTCTC	CTTAGAAGTT	CCATACACAA	CACATCTCCC	TAGAAGTCAT	TGCCCTTACT	60
TGTTCTCATA	GCCATCCTAA	ATATAAGGGA	GTCAGAAGTA	AAGTCTGGNT	GGCTGGGAAT	120
ATTGGCACCT	GGAATAAAAAA	TGTTTTCTG	TGAATGAGAA	ACAAGGGAA	GATGGATATG	180
TGACATTATC	TTAAGACAAC	TCCAGTTGCA	ATTACTCTGC	AGATGAGAGG	CACTAATTAT	240
AAGCCATATT	ACCTTTCTTC	TGACAACCAC	TTGTCAGCCC	ACGTGGTTTC	TGTGGCAGAA	300
TCTGGTTCTA	TAACAAGTTC	CTAATAAGCT	GTAGCCAAA	AAATTGATG	AGGTATTATA	360
ATTATTTCAA	TATAAAGCAC	CCACTAGATG	GAGCCAGTGT	CTGCTTCACA	TGTTAAGTCC	420
TTCTTTCCAT	ATGTTAGACA	TTTCTTGAA	GCAATTAG	AGTGTAGCTG	TTTCTCAGGT	480
TAAAATTCTT	AGTAG					495

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TATGGTTGCC TATTCTTGT	60
ACAGTAAC	
TC AACTGATCTA GGAAAGAAAA AATGTTTGT	
CTTCTAGAGA TAAGTTAATT TTTAGTTTC TTCCCTCCTCA CTGTGGAACA TTCAAAAAAT	120
ACAAAAAGGA AGCCAGGTGC ATGTGTAATG CCAGGCTCAG AGGCTGAGGC AGGAGGATCG	180
CTTGGGCCA GGAGTTACA AGCAGCTTGG GCAACGTAGC AAGACCCCTGC CTCTATTAAA	240
GAAAACAAAA AACAAATATT GGAAGTATTT TATATGCATG GAATCTATAT GTCATGAAAA	300
AATTAGTGTAA AAATATATATT ATTATGATTA GTTATCAAGA TTTAGTGATA ATTTATGTTA	360
TTTTGGGATT TCAATGCCTT TTTAGGCCAT TGTCTCAAAA AAATAAAAGC AGGAAAACAA	420
AAAAAGTTGT AACTTGAAAA ATAAACATTT CCATATTAT AGCCAAC TAA GTGGGTTTNG	480
GGTNGGTTGG GTTGGTTGGT	500

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TTATCATTAA CAGGTCCCAC AACCTTAAA AAGTACAGAT TTTTTTTTTC TTNGTGGAGA	60
CAGGGTCTCA CTTGGTCGCC CAGACTGGAG TGCAGTGGCA CGATCTCAGT TCACCACAAAC	120
CTCTGCCTCC TGGGTTCAAG CAATNCTCGT GCTTAAGCCT CCTGAGTAGG TGGAACCACG	180
CGTGCACGCC ACCACGCTAG GTTNATTGTG GCTTTTTAG TAGAGACAGG GTTTCGCCAT	240
GTTGCCAGG CTGGTCTCAN ATTCCNGACC TCAAGTGATC CGNCCGCCTC AGACTCCCAA	300
AGTGNTGAGC ATTACAGNTG TGTACCACTA TGTCCNGNC CNCATCTCTC TTTAAAACAN	360
CTTNCATTAA CCTAGTCCAC TCCTG	385

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GACCTAGAAA AGAAAGCATT TCAANNTAAT TAACAGGTCC CACAACCCTT AAAAAGTACA	60
GATTTTTTTT TTCTTTNNGG AGACAGGGTC TCACHTTGTC GCCCAGACTG GAGTGCAGTG	120
GCACGATCTC AGCTCACCAC ANCCTCTGCC TCCTGGGTTA AAGNANTTCT CGTGCTTANG	180
CCTCCTGAGT AGGTGGAACC ACGCGTGTGC GCCACCACGC TAGGCTACTT TNTGTATTT	240
TAGTAGAGAC AGGGTTTCGC CATNTTGCCC AGGCTGNTCT CAAATTCTG ACCCNCAAGT	300
GATCCCCCCTT CTTCAAGTAC TCCCCATCAG	330

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GGTGGNCGTT CTAGAACTAG TGGCNCCAA GGNAGAAGAA GTTTCTTAG TACAGAACAA	60
AATGAAANGT CTCCCATGTC TACTTCTTTC TACACAGACA CGGCATCCAT CCGTTTTCT	120
CANTCTTCC NCCACCTTTC CCGTCTTCT ATTCCACAAA GCCGNCATTG TCATCCTGGC	180
CCNTTCTCAA TGAGCTGTTG NNTACACCTC CCAGACGGCG TGGTGGNCGG TCAGAGGGGC	240
TCCTCACTTC CCAGTAGGGG TGGCCGNNGCA GGNNGGTGCCC CNCACCCCCC GGGCGGGGTG	300
GTTNGTCCNN CCGGNGGGNT GCACCNCCCC CACCCCTCCC CNCTCTNCTA CTGGCGGTG	360
TNTATTNCAN NATTTAAG CA	382

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GGATCCAAAG GAAGTTAGAG GCCAGCTCAG TCTACACCTG CTACTGNTCA GTGCCACCC	60
GGTCAAGGGA GACCAACACA TGGTAAAGGT CAAGGGCTTC TTGGAAGGCA GTCAGCAGCC	120

TGTGCAAGAT GTTCTCCACA CTGCTCAGNT TAAGGGGAGC TGGGGGCAGG ACCTCAGCTG	180
GNATCTCTGC TTCACCCAGTG TCCAGGGGTT GCACAATTCT TGTTTACTCG TAGGATATT	240
AATCTTGGNN GGTGCTATCA TAAATGGGAC TTATCCNCTN ATTATGTTTT CTTACTAGTT	300
GTTTATGTGA AGGTTATTGA TTTGGGTTTC ACTTTATTN GTGGNAATGG AGTTTCAC	360

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AATGTCACGG ATTCCCTTAG GTAGNTACAC CCATCAACCT TTTTGAGAAT AAAATGAATT	60
GAGAGTGTAA CAGTCTAATT CTATATCACA TGTAACCTTT ATTTGGATAT ATCAGTAATA	120
GTGCTTTTT TTTTTTTTT TTTTTTTTNG GNGANAGAGT CTCGCTCTGT	180
CGCCAGGTTG GAGTGNAATG GTGCGATC	208

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AACAAGGTTT CTCGGTCGGC GGTGAATATA CCGGGGCGTC GATATTGTT GCGGAATACT	60
CCCCTGACCG TAAACGTGGC TTTATGGGCA GCTGGCTGGA CTTCGGTTCT ATTGCCGGGT	120
TTGTGCTGGG TGCAGGCGTG GTGGTGTAA TTTCGACCAT TGTCGGCGAA GCGAACTTCC	180
TCGATTGGGG CTGGCGTATT CCGTTCTTA TCGCTCTGCC GTTAGGGATT ATCAGGCTTT	240
ACCTGCGCCA TGCAGCTGGAA GAGACTCCGG CGTTCCAGCA GNATGTCGAT AACTGGAAC	300
AGGGCGACCG TGAAGGTTTG GAGGATGGCC CGAAAGTCTC GTTAAAGAG ATTGGCACTA	360
AATACTGGNG CAGNCTGTTG AATGTTGGG CTTGGTAATT GGCAACCAAC GTGATTACTA	420
NATGTTGGTG ACCTATATTG CCGAGTTATT GGCGGATAAC CTGAATTATC	470

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 440 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TAATTATATT GAAATGCTTC TCNTCTAGGT CATCCATGNC TGGNTTATTA TATCATCTCT	60
ATTGNTGNTG CTCTTTTTA CATNCATTTA CTTGGGGTAA GTTGTGAAAT TTGGGGTCTG	120
TCTTCAGAA TTAACTACCT NNGTGCTGTG TAGCTATCAT TTAAAGCCAT GTACTTTGNT	180
GATGAATTAC TCTGAAGTTT TAATTGTNTC CACATATAGG TCATACTTGG TATATAAAAG	240
ACTAGNCAGT ATTACTAATT GAGACATTCT TCTGTNGCTC CTNGCTTATA ATAAGTAGAA	300
CTGAAAGNAA CTTAAGACTA CAGTTAACCTA TAAGCCTTG GGGAGGATT ATATAGCCTT	360
CTAGTAGGAA GTCTTGTGCN ATCAGAATGT TTNTAAAGAA AGGGTNTCAA GGAATNGTAT	420
AAANACAAA AATAATTGAT	440

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AAAACAAAGC CTCTTGAGGT TCTGAAAAGG GAAAGAAAAA CAGAACTTTG TGCAC TACAA	60
TTATACTGTT ATAAAAAAACA CTTCCATAGA TTACATTAAG CAGAAACAAA CCTTTCTTTC	120
ATGTGTTCTC CTCCAGGCCA AGCTGTCTAA GGACCGCAAA GGCTGTTGTC ACTTGCAGGC	180
TCCCAGATTA GGTCTGAAAT AGGATTCAC CAGGTCA TCC ATTGTTAGTT AAATCCTAGT	240
AAATTCA TTT ANACCAATCA AATACTTATA AGACCAATT GTAAACCAGG AATGTATTAA	300
TTTGTACGA CTTTCAACTA ACTGACAAAT TTACTATAAG CTCAAGGTAG GACTCTTCTAG	360
CAATAAGTAG GAACCGCCTG AGACAACCAA ACATTTCAA CCCACAAANG ATACTTTAAT	420
GACTTTCTGA TTTNCCAGCA AAAGGGGGG	449

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGATCCGCC CTCCTCGGCCT CCCAAAGTGT TGGGATTACA GGCGTGAGCC ACCGCACCTG	60
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GCTTTTTTTT TTTTTTTTT TGGNGGAGAC AGAGTCTTAC TCTGTTGCC AAGCTGGAGT	120
GCAGTGGTGC AATCTGGTT CACTGNAACC TCCACCTCCA GAGTTCAAGC AATTCTCTGC	180
CTCAGTTCT GGAGTAGCTG GGATTACAGG TGCCTGCCAT CACGCCTGGC TAAATTTGGN	240
ATTTTTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGGTCTT GAACTCCTGA	300
CCTTGTGATC CACCAGCCTC GGCCTCCAA ATTGNTGGGA TTACAGGCGT GAGCCACCAC	360
AACCAGGCTA AAGTTTAAA ACATGCCAAG TGTATTTACA TAATGCGATA CGANTTATGT	420
ACATA	425

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGATCCGCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTNTTGTAA AATAAGCATG TTATCTGTCC NNCCTGCCTT	180
GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC	240
AAATGATTT ATGAAAATAT AAAGATTAGN TTGAGTTGG GCCAGCATAG AAAAAGGAAT	300
GTTGAGAACCA TTCCNTTAAG GATTACTCAA GCTCCCTTG GTGTATATCA GNNGTCANNA	360
CNTATCTTNG GGGCTGAAAA ATGTTT	386

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAAAAGGGAA AGAAAAACAG AACTTTGTGC ACTACAATTA TACTGTTATA AAAAACACTT	60
CCATAGATTA CATTAAGCAG AAACAAACCT TTCTTTCATG TGTTCTCCTC CAGGCCAAGC	120
TGTCTAAGGA CCGCAAAGGC TGTTGTCACT TGCAGGCTCC CAGATTAGGT CTGAAATAGG	180
ATTTCACCAAG GTCATCCATT GTTAGTTAAA TCCTAGTAAA TNCA	224

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGATCCGCC	TCCTCGCCT	CCCAAAGTGT	TGGGATTACA	GGCGTGAGCC	ACCGCACCTG	60
GCTTTTTTT	TTTTTTTTT	TGGNGGAGAC	AGAGTCTTAC	TCTGTTGCC	AAGCTGGAGT	120
GCAGTGGTGC	AATCTTGGTT	CACTGCAACC	TCCACCTCCA	GAGTTCAAGC	AATTCTCTGC	180
CTCAGTTCT	GGAGTAGCTG	GGATTACAGG	TGCCTGCCAT	CACGCCTGGN	TAAATTTGGG	240
ATTTTTTTT	AGTAGAGACA	GGGTTTCANC	ATGTTGCCA	GGNTGGTCTT	GGACTCCTGA	300
CCTGGTGAAC	CACCAGGCTC	GGGCTCCAAA	TTTGGTTGGG	ATTACAGGGG	GTNAANCAAC	360
CACAACCCAG	NCTAAAGTTT	TNAAAACATN	CAAAGTGT	TAAAATNATG	NGATACGATT	420
TATTGTACAA	TTAATT	TTAT				440

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTCTTCCCA	TCTTCTCCAC	AGAGTTGTG	CCTTACATTA	TTACTCCTTG	CCATTTCAA	60
GAAAGCATTG	TCAGCTCTTC	CAATCTCCAT	CACCTTG	GGCTTCT	ACTTTGCCAC	120
AGATTATCTT	GTACAGCCTT	TTATGGACCA	ATTAGCATT	CATCAATT	TT ATATCTAGCA	180
TATTTGCGGN	TAGAATCCCA	TGGATGTTTC	TTCTTGACT	ATAACAAAAT	CTGGGGAGGA	240
CAAAGGTGAT	TTCCCTGTGT	CCACATCTAA	CAAAGTCAAG	ATCCCCGGCT	GGACTTTGG	300
AGGTTCTTC	CAAGTCTTCC	TGACCACCTT	GCACATTGG	ACTTTGGNAA	GGAGGTGCCT	360
ATAGAAAACG	ATTTGGAAC	ATACTTCATC	GCAGGGGGAC	TGTGTCCCC	GGTGGCAGAA	420
NCTACCAAGA	TTTGC	GGGNC	GAGGTCAA			448

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGATCCGCC	GCCTTGGCCT	CCCAAAGTGC	TGGGATTACA	GGCATGAGCC	ACCGCTCCTG	60
GCTGAGTCTG	CGATTCTTG	CCAGCTCTAC	CCAGTTGTGT	CATCTTAAGC	AAGTCACTGA	120
ACTTCTCTGG	ATTCCCTTCT	CCTTNAGTAA	AATAAGNATG	TTATCTGNCC	GCCCTGCCTN	180
GGNNATTGNG	ATAAGGAT					198

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTGCAGTGAG	CCGTGATTGC	ACCACTTAC	TCCAGCCTGG	GCAACAAAAT	GAGACCCTGG	60
CTCAAAAACA	AAAACAAAAA	CAAAAAAAGA	GTAAATTAAT	TTAAAGGGAA	GTATTAAATA	120
AATAATAGCA	CAGTTGATAT	AGGTTATGGT	AAAATTATAA	AGGTGGGATA	TTAATATCTA	180
ATGTTGGGA	GCCATCACAT	TATTCTAAAT	AATGTNTTGG	TGAAAATTAT	TGTACATCTT	240
TTAAAATCTG	TGTAATTTTT	TTTCAGGGAA	GTGTTAAAAA	CCTATAACGT	TGCTGTGGAC	300
TACATTACTG	TTGCACTCCT	GATCTGGAAT	TTTGGGTGTG	GTGGGAATGA	TTTCCATTCA	360
CTGGAAAGGT	CCACTTCGAC	TCCAGCAGGC	ATATCTCATT	ATGATTAGTG	CCTCATGGNC	420
CTGGTGTAA	TCAAAGTACC	TCCCTGAATG	GACTGCGTGG	GTCATCTTGG	NTGTGATTCA	480
GTATATGGTA	AAACCCAAGA					500

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CTGCAGCCTT	GACCTCCTGG	GATCAATCGA	TCCTCCCACC	TCAGCCTCCT	AAGTAGCTGG	60
AACTACAGGT	GTGCACCACC	ATGCCCGGCT	AATNGNTGTA	TTTCTGTAG	ATACGAGGTN	120
TNGCCATGTT	GCCCAGGCTG	GTCTTGAACT	CTGGGCTTAG	GTGATCTGCC	CGCCTCAGCC	180
TCCCAAAGTG	CTAAGATTAC	AGGCATGAGC	TACCATGCC	AGCCGAAATC	TTCAAATGAA	240

AAAGTTACTA TAGCTAATTA ATGATTACT GAAGAGTTAT GGGATGTACA CGTTACCATT	300
TTCTCTAAAT CAAGATAAAG AGATGAGGAA AGAAAACACT CCAGTGGGC ATTCTGTNA	360
CAAAACAAAT TATCAGTCTT GGGGTTTNA CATATACTGA AATCACAGGC AAGATGAGCC	420
ACGCAGTCCA TNCAGGGAGG TACTGGATAA CACCAGGGNC ATGAGGGACT AATCATAATG	480
AGATATGCTG CTGGAGTCGA	500

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTGCAGGATG AGAGCGATCT CTTNTTNCAT TTCCCTGCGCT ACGCGCTGCG GGCGACCAA	60
TTCTTCGCC ATAATAAATT CTCCTGACNA AAAAGGGGCT GTTAGCCCT TTTTAAAATT	120
AATTCAGGT GGAAGGGCTG TTCACGTTGA CCTGATAAGA CGCGCCAGCG TCACATCAGG	180
CAATCCATGC CGGATGCAGC GTAAACGCCT TATCCGCAT GGAACCTAA AACCTTAAG	240
CAATGGTACG TTGGATCTCG ATGATTCGA ATACTTCGAT CACATCGNCA GTGCGGACGT	300
CGTTGTAGTT CTTAACGCCG ATACCACATT CCATACCGTT ACGGGACTTC GTTAACGTCA	360
TCTTTGGAAG CGGGGCAGGG ACTCCAGCTC GNCTTCGTAG ATAACCACGT TGGCACGCAG	420
GAACGCGGGT CGGGTTGTGA CGTTAACAC AACTTCCGGG TAACCATACA GGCTGNGATG	480
GNACCAAATT TCGGGGGATT TGGACAAGTC AAGAACTTCC CGCCAGACCG ATAATCTTGT	540
TGTTCAAGTTC	550

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CTGCAGCTTT CCTTTAAACT AGGAAGACTT GTTCCTATAC CCCAGTAACG ATACACTGTA	60
CACTAAGCAA ATAGCAGTCA AACCCAAATG AAATTTNTAC AGATGTTCTG TGTCACTTTA	120
TNTTGTCTAT GTTGTCTCCC CCACCCCCAC CAGTTCACCT GCCATTATT TCATATTCA	180
TCAACGTCTN NNTGTGTAAA AAGAGACAAA AAACATTAAA CTTTTTCCT TCGTTAATTC	240

CTCCCTACCA CCCATTACCA AGTTAGCCC ATACATTTA TTAGATGTCT TTTATGTTT	300
TCTTTNCTA GATTTAGTGG CTGNGTTGTG TCCGAAAGGT CCACTTCGTA TTGCTGGTTG	360
AAACAGCTCA GGAGAGAAAT GAAACGCTTT TTCCAGCTCT CATTACTCC TGTAAGTATT	420
TGGAGAATGA TATTGAATTA GTAATCAGNG TAGAATTAT CGGAACTTG AAGANATGTN	480
ACTATGGCAA TTTCANGNA CTTGTCTCAT CTTAAATGAN AGNATCCCTG GACTCCTGNA	540
G	541

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

NNCCNCNCN NNNNNNNNTN NTNTGCCCG ATAACATAG GGNGACTTGG AGATCCACCG	60
CGGTGGCGGN CGNTCTAGAA CTAGTGGATC CCCCGGGNTG CAGGACCCAA CGCTGCCCGA	120
GATGCGCCGC GTGCGGTTGC TGGAGATGGC GGACGCGATG GATATGTTCT GCCAAGGGTT	180
GGTTTGCAGCA TTCACAGTTC TCCGCAAGAA TTGATTGGCT CCAATTCTTG GAGTGGTGAA	240
T	241

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 834 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CCCCCCCNCN NNNNNNTTTN NGCAGCCCGT AATTACCCTC ACTNCCGGGA ACAAAAGCTG	60
GGTACCGGGC CCCCCCTCGA GGTCGACGGT ATCGATAAGC TTGATATCGA ATTCTGCAG	120
TGTTTAAAAA ATAAAATAAA CTAAAAGTTT ATTTATGAGG AGTACACTGC TTTCTTGTAA	180
ACACATGTAC AAGCCATATA ATAGAGTTCA TTTTTTACCC TAGTTACGGA AACACTAGAA	240
AGTCTTCACC CGGCCAAGAT AACACATCTT TAGAAAAAT AGCAAGAAAT ATTTTATGGG	300
TTGTTTACTT AAATCATAGT TTTCAGGTTG GGCACAGTGG NTCATGCCTG TAATCCCAGC	360
ACTTTATGCG GNTGAGGCAG GCAGATCAGT TGAGGTCAGA AGTTGGAGA CCAGNCTGGG	420
CAATGTGGNA AAACCTCATC TCCACTAAAA ATACAAAAAT TAGNCAGGCA TGGTGGTGCA	480

CACATGTAAT TCCAGNTACT TGGGGAGGCT GAGACAGGAG GATCGNTTGA ACCTAGGGAG	540
GGAGGAGTTG GAGTGAGCTA ATGTCAATGC ACTCTTGGTT GGGGCGANAG AGCAAGATCT	600
TTCTTCCAAA AAAAAAAA AAAAAAAAGC CAGGTGNGGN GGTCAAGGCT GTAATCCAGA	660
ATTNGGGAGG CCGNGGAGGN NATCANTGNG GNAGGGNTCA AGNGGGCNG GCCACATGGG	720
GAACCCGTTN TTNTTAAATN AAAATTAGCC GGGGNGGGG AGGACTNTAT CCNGTTCCGG	780
NGGTGNGGAG GATCNTTATT NTGGNGGAGG GTGGATGNNC CAGTTGACNC CCCC	834

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 838 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTGGGCNCNC GCCCCTTAAN TTTTTATNGN TTNCTANAAA AANANNNGGC NCNNNTAAAAT	60
ATATTTTTTN TTGTGACCCC TTTTAAAAGG GACCCNCTAA AAAATTTNT GGTTNNNTTN	120
GATTTANGTG GGTGNTTTN TTATATTTTT GGNGAGNNTC TGTAGTCNTC NCCCTCAAAC	180
ANNTCNTACN ATNGGNANCG TGACTCTGTC NTTNGTNANN NTCGNTNTCN NGTNATTCNA	240
GGNNCCTCGC GCNNCNCGGG CNNNGTTTT TTTNNCNNTT TTTAAGCCNA ANNCTCAGTA	300
NCNTCCAACG GNGCTNNGAC ANNNGNNNCT NTCGNGGTN CCCTCTNTNT NGNNCNNGGC	360
TNNNGNNNNC NGNCNGCNGN GCCNTGCGNN NNGNNNGNGG NNNGNNTNNCA TANGGATNGN	420
GNTGCTCNNC NCNNNGNTNN TNAGTAGGNA NTTTTNTNNNT ACTTGCCNNC NNNTNGCTGC	480
GAGNANAGCN ANNTNGNNGN AGNGNNGNTG CGCGGANNTT CCCCTGATNA NCTCGAGCNG	540
NTTACNGGNG CNNCCTNGAA NAAGNGNNGT ANNGTGCCGA GNCGCTANN C TGAGCCTGAG	600
TNTCGACNGG NATNGTGNNT CNTACNGTTA NGGGNNGCNN GANCGGNTG ANTNCNCCGGN	660
NGANCNAGCG ACTGCCTNTC ANGCGAANCG TNTCANGNNN GTAGAGCANA GGGTNANNNG	720
TCNNNNAAAGC NTNNAGTGAN TGTCTNACN NGTGANNTAC GGCNTAGNCT TGATNTNNAN	780
NCGAGGNNNN ATNNANNNTT GGANANTTNN TNNNNTCNCN TCGCGGNGNG NCNNNGCCG	838

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 803 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATTCGCGCGT AGCCCGATAA CTATAGGGCG ACNTGGAGNT CCACCGCGGT GGCGGCCGCT	60
CTAGNAACTA GTGGATCCCC CGGGCTGCAG GAATTACGG ACTAATCCTC TACAGATCTT	120
GCTGGAGTGG CCTTCAGCC TTTTGTGACT GTTTGTAGTG AAATGTACAC ACAAGCCTAC	180
AAGGCAGCCC AGATGTACCA TAACTGTGGG AAAATTAAAA AAAAAAAAAC ACAGAACCTC	240
TCTATGTTGC CCATGCTGGA CTCAAACTCT TAGACAAGCA ATCCTCGTAC CTCAGCCTCC	300
TGAGTTCCCTG AGTAGCTGGG ACTACAAGCA TGCAACACCA TGCCAGGCTA TGAGAAAGTT	360
CTTTTATTG ATCCAGACCT TATTGCCTGG TAACTTCCAC CACTGTTCCCT AGCTCTGNTC	420
TCTGGTCCTA ACAGAGGAAA ATCTTGACCC CACACCTAGT GCAACTGGAT AGCTTATNGT	480
TGGGCTNGTG TTTCCTCTAT TCTGGGTCCA CCCTAAAATC CNATAGATAAC TCCAACGTCT	540
CANAGNAAAC CAAGCTCTCT CTCTNNCTTN CTTTCTTNNNN CTCTATTNAT TNATGGGNNA	600
TNATTNATTN NGGGGATGGN GTTCGGTCGC CGCCCGGCTG GNGTGAAATG GGGGAGGCAA	660
TCAATTAAAC CCCACCCNGG GTCCAGGGAT CTCGTTNAAA CCGNNNNNNN NNNNNNNNNNA	720
NGNNCCNCNC NNNCCNNTNN NNNGTTTNN NNGNNNNNGG NNNCCNNNN NANNNNNNNTN	780
NNNCCNCCNA NNNTNCNNNN CCC	803

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CNNNNNNNNCC CNNTNATTNT ACGCCAGCCG CGTAATTAAC CCTCACTAAA GGGAAACAAAA	60
GCTGGGTACC GGGCCCCCCC TCGAGGTCGA CGGTATCGAT AAGCTTGATA TCGAATTCCA	120
ACTCCTCACT TGCCAGATGT GACCTTAAGC AAGTGAACCTT CTGTGTGCCA CACTGTTTC	180
ATCTGTAAAA GGATAAAGGG AATATCATAA ATTAGNTTGT TAAGCCTTAG TTTAATAATG	240
TCTCTAAGTT TTACATATAA GTAGACAGTG TCTTTCTTGT TTAGTGAATA ATCATTCTTA	300
TTATTTAATA GTATCTCTAC TAAATTATT GTGTAAGATT ATACTAATCT TGTTTAGTGC	360
GTGGTAATCA CTTCTGCTCA TATTAAACCT ATAAGCATAA TATAGTTTAT TTATATACCA	420
NTTATTTATT TTATTTATT TGNNGAGATG CAGCTTGTCT TTTNCAACCC AGGGNTGNNG	480
NGNAGNNGNG NAANCTTGNT TCACTGNAAC CNCCACCNCC CAGGTNCAAG NGATTCTCCT	540
GNTCAAGCCN CCTNAGNAGN TGGNATTACA GNACGANTAC ANNCCAGNTA NNNNGGNTNT	600
NNGNTNGNNA GGNNNCACAN NNGNCAGGTN NNTCGNCTCC NNGCCANTNA CTNNNNCCAN	660

CCCCNNNGNN NNNNATANAG NATNANCANN NNCCNCNNN NCNNNNNNNG GNGGANCCN	720
NTNGCNGNN ANNGNNANNN NNTNNNNNNN NNGNCNNNG NNNNNNNNCC NNNNNNNCC	780

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

NNNNNNNNNC CNNNNNNTTC GNNGTAACN CGANTCACTA TAGGGCGACT TGGAGCTCCA	60
CCGCAGGTGGC GGCCGCTCTA GAACTAGTGG ATCCCCGGG CTGCAGGAAT TCGATATCAA	120
GCTTTNGTGT GTAAAAAGTA TTAGAATCTC ATGTTTTGA ACAAGGTTGG CAGTGGGTTG	180
GGAGGAGGGA TTGGAGATTG ATGCGATAGG AATGTGAAGG GATAGCTTGG GGTGGATT	240
ATTTTTAAT TTTAATTTC ATTNTTGAG ATGGAGTCTT GCTCTGTCTC CCAGGCTGGA	300
GTGCAGTGGT GTGATCTCAG CTCACGGTT CAAGCGATTC TCCTGCTGCA GCCTCCCGAG	360
TAGCTGGAT TACAGGAGCG CGCCACCACA CCCGGNTAAT TTNNNTGTAT TTTTAGTAGA	420
GACGGGGTTT CACCATGTTG GTTAGGCTGG TCTAGAACTC CCAACCTCAT GATCCGCCTG	480
CTTCGGCCTC CCAAAGTGCC GGAATTACAG GCGTGAGCGA CTGCACCCGG CCGCTTGGG	540
GTGGATTTT AAAGAAATT AGAAGAATGT AACTTGGCCA GATACCATGT ACCCGTTAAT	600
TCATTTNCGG TTTTTGGAT ACCCATTTC NNATTCTCCC NCCACTGGAT AAATAAGGGN	660
GGTTCATTNT NGNTTAGTTT GGGTNTTTT NAGTGTGGNT TCTGCTTATN ATTAGAATGG	720
NCTNCTTNC CAANCTGGAA AGGGAGGAGT TAAAATCANT ACCAGAANCA GAAATTCTTT	780
TCANTTGTG CNCNAGAAAT GCC	803

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TNCCNNNNCN NNNNNAATT TNGCAGNCGC GTAATTAACC TCACTAAAGG GAACAAAAGC	60
TGGGTACCGG GCCCCCCCCTC GAGGTCGACG GTATCGATAA GCTTCCCTCC CCTTCCTCAG	120
CTCTGGCGAC CCTGCGCTGT GGTGGTTCTC CAACCACACT CATTCTCCTC AGCTGGCTCC	180
TTGCTCTTCT TCCACCCCT CGTTGGAAGT GTTCCTAAGT GTTGGCTTG GCCTCCTCT	240

CCCCCTTCCTT AGNTTAGACT TCTCCACTGC TCCAACATCA ACTGGAAATC TATGGAATTG	300
ATTCCTGTTT TCAGCTCCAG TCCTGTTCAC AGGGCATTTC CACCTGCTGG CACTTCCAAA	360
GTGACACTTC CAAACCACCTT CCTCGCCCTC CTCTCTAACAC CAGGTCTTTC TTCCTAACTT	420
CCTTATTCTC GAGAATGTCT CTGNATGTT CTAAACTGAA AACTCCTAGT CAACTNCACA	480
CTTTATTCCC TGGATCCTCA ATTGGGTTCC CATGTNCCGT TAGTGTTCCT TGGTAAGNCT	540
CTGCCANACAC CGNAGGATCG ACTCTAATCA CATCTCAACT GAATTATGGN AAAGTCAACT	600
CAATTCTCTC AACCATCCCA GGCTCCACTA TGGNTAATAT GCTAAGGAGA GCTGACCCAA	660
CGGGGAGAAG ATCTGNGGG GAGGAGAGAA ACAAAAGNTAA TGGAATNATT CTCGAAAAGC	720
CCACAAAGGNG AAGGATAACC CNCTCCNCT CGAAAGAGGG GGGATCGCCA GATNTCGCGC	780
CCGGAAAGAA ACCGGGGNGA GGGGGTTACA NTGTAAGNC	819

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 796 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TNTTGGCTGG TACTGCTTGA GCAACTGGTG AAACCTCCGCG CCTCACGCC CGGGTGTGTC	60
CTTGTCCAGG GGCGACGAGC ATTCTGGCG AAGTCCGCAC GCCTCTTGTGTT CGAGGCGGAA	120
GACGGGGTCT GATGCTTCT CCTTGGTCGG GACTGTCTCG AGGCATGCAT GTCCAGTGAC	180
TCTTGTGTTT GCTGCTGCTT CCCTCTCAGA TTCTTCTCAC CGTTGTGGTC AGCTCTGCTT	240
TAGGCATATT AATCCATAGT GGAGGCTGGG ATGGGTGAGA GAATTGAGGT GACTTTCCA	300
TAATTCAAGGT GAGATGTGAT TAGAGTTCGA TCTGCCGTGG TGGCAGAGGC TTACAAGAAA	360
CACTAACGGG ACATGGGAAC CAATTGAGGA TCAGGGAATA AAGTGTGAAG TTGACTAGGA	420
GGTTTTCACT TTAGAACATG GCAGAGACAT TCTCAGAAAT AAGGAAGTTA GGAAGAAAGA	480
CTGGTTTAGA GAGGAGGGCG ANGAAGTGGT TTGGGAAGTG TCACCTTGGG AAGTGCCAGC	540
AGGTGAAAAT GCCTGTGACA GGATGGAGCT GAAAACAGGA TCAATTCCAT AGATTCCAGT	600
TGATGTNGGA GCAGGGGAGA AGTCTTAGCT AAGGAAGGGG AAGAGGAGGC CAAGGNAACA	660
CTTAGGACAA TTGNAACGAN GGGGGGGAG AAGAGNAAGG GCCACTTAGG GGAATAATNT	720
GGTGGGGGAC CCCAAGNNA GGGCGCANNN TTAGGAGGGG GGGANNTCAN AGGAAAGTGG	780
AAGNTTGGGT TTANCT	796

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATTCGTCGTA	NCCCGATNAC	TATAGGGCGA	CTTGGAGCTC	CACCGCGGTG	GCGGNCGCGG	60
GCAGGGNCCG	GNCCTTGTG	GCCGCCGGG	CCGCGAAGCC	GGTGTCTAA	AAGATGAGGG	120
GCGGGGCGCG	GNCGGTTGGG	GCTGGGAAAC	CCCCTGTGGG	AAACCAGGAG	GGGCGGCCCG	180
TTTCTCGGGC	TTCGGGCGCG	GCCGGGTGGA	GAGAGATTCC	GGGGAGCCTT	GGTCCGGAAA	240
TGCTGTTGC	TCGAAGACGT	CTCAGGGCGC	AGGTGCCTT	GGCCGGGATT	AGTAGCCGTC	300
TGAACCTGGAG	TGGAGTAGGA	GAAAGAGGAA	GCGTCTTGGG	CTGGGTCTGC	TTGAGCAACT	360
GGTGAAACTC	CGCGCCTCAC	GCCCCGGGTG	TGTCCTTGTG	CAGGGGCGAC	GAGCATTCTG	420
GGCGAAGTCC	GCACGCCTCT	TGTCGAGGC	GGAAGACGGG	GTCTTGATGC	TTTCTCCTTG	480
GGTCGGGGAC	TGTCTCGAGG	CATGCATGTC	CAGTGACTCT	TGTGTTGGT	GNTGCTTCCC	540
TCTCAGATCT	TCTCACCGNG	GTGGGCAACT	CTGTTAGGC	ATATTATCCA	TAGNGGAGGC	600
TGGATGGTTG	AAANAATTGA	GGTNATTTC	CATAATCAAG	TGAAATTGGA	TAGAGTCCGN	660
CTTNNGGGT	GNAAGGGTTA	AAAAAAAATA	ACGGAAATGG	AACAATGAGG	TCAAGGATTA	720
GTTGAGTTGN	TAGNGGTTCA	ATTAGANATG	AAGGNATCTA	AAATAGGAGT	AGAGAANNNG	780
TTNAAAGAGG	AAAAATTTC	CC				802

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

ATATGCAGCC	GCGTAATTAA	CCTCACTAAA	GGGAACAAAA	GCTGGGTACC	GGGCCCCCCC	60
TCGAGGTCGA	CGGTATCGAT	AAGCTTGATA	TCGAATTCT	GCAGCCCGGG	GGATCCGCC	120
CGCGGCCTCC	CAAAGTGCTG	GGATTACAGG	CGTGAGCCAC	CGCCCCGGGN	CTCACATTTC	180
ATTTCTATTG	GCTAGCGCTG	CTCTAAATCT	TCTGTTCTT	CTGCTACACC	AGGCCTAACAA	240
CTCAAAATCC	CTGCCAACCT	TTTCCTTCCT	GAAGCTTCCC	TCCCCTTCCT	CAGCTCTGGC	300
GACCCCTGCGC	TGTGGTGGTT	CTCCAACCAC	ACTCATTCTC	CTCAGCTGGC	TCCTTGCTCT	360
TCTTCCACCC	CCTCGNTGGA	AGTGTTCCTA	AGTGTGTTGGC	TTGGCCTCCT	CTTCCCCCTTC	420

CTTAGCTTAG ACTTCTCCAC TGCTCCAACA TCAACTGGAA ATCTATGGAA TTGATTCCCTG	480
TTTCAGCTCC AGTCCTGTT ACAGGGATT TTCANCTGGT GGCATTCCA AAGTGAAATT	540
CCAAACCACT TCCTCGGCCT CCTCTTCTAA ANCAGGTCTT TCTTCCTAAC TTCCTTATTC	600
TTGAGAATGT CTCTGCATGT TCTTAAANTG AAAACTCCTA GTCAAATTCA AATTATCCC	660
TGATCCAAA TGGTCCCATT CCCGTAGGGT TTNTGTAGCC TGCACACCGA GGTGGANTT	720
TATNNATTCA CCGATTATGG AAAGTAACCA ATCTTNACCA NCCAGCTCAT TTGTTNTNTG	780
CTAAGAGGGT NCC	793

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 440 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

AAAGTCATGG ATTCCTTAG GTAGCTACAT TATCAACCTT TTTGAGAATA AAATGAATTG	60
AGAGTGTAC AGTCTAATTC TATATCACAT GAACTTTA TTTGGATATA TCAGTAATAG	120
TGCTTTTCN TTTTTTTTT TTNTTTTTT TNNTTTNGG GGAGAGTC TCGCTCTGTC	180
GCCAGGTTGG AGTGCAATGG TGCGATCTTG GCTCACTGAA AGCTCCACCN CCCGGGTTCA	240
AGTGATTCTC CTGCCTCAGC CNCCCAAGTA GNTGGGACTA CAGGGGTGCG CCACCACGCC	300
TGGGATAATT TTGGGNTTT TAGTAGAGAT GGCGTTTCAC CANCTGGNG CAGGCTGGTC	360
TTGGAACTCC TGANATCATG ATCTGCCTGC CTTAGCCTCC CCAAAGTGCT GGGATTNCAG	420
GGGTGAGCCA CTGTTCTGG	440

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTTAGTCTGT NTCGTAGTCA TATTAATTGT AAGTNTACAC TAATAAGAAT GTGTCAGAGC	60
TCTTAATGTC AAAACTTTGA TTACACAGTC CCTTTAAGGC AGTTCTGTT TAACCCCCAGG	120

TGGGTTAAAT ATTCCAGCTA TCTGAGGAGC TTTTNGATAA TTGGACCTCA CCTTAGTAGT	180
TCTCTACCCCT GGCCACACAT TAGAATCACT TGGGAGCTTT TAAAACGTGA AGCTCTGCC	240
TGAGATATTCTTACTCAATT TAATTGTGTA GTTTTTAAAA TTCCCCAGGA AATTCTGGTA	300
TTTCTGTTA GGAACCGCTG CCTCAAGCCT AGCAGNACAG ATATGTAGGA AATTAGCTCT	360
GTAAGGTTGG TCTTACAGGG GATAAACAGA TCCTTCCTTA GNCCCTGGGA CTTAATCACT	420
GAGAGTTTGG GTGGNGGTTT NGNATTAAAT GAC	453

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GACACACATT CACACATAAT TATGAAAGCA TTTTCAGGCA AACTCAATC ACAAGTCTGG	60
GTTTTTAACATAGTTAACTG AATATTTCCC TTGGGGGGTT AAATTTAGA ACAGACGTNC	120
ATNCAATCTG GAAGAAGAGC TATGAAAAAA ACCTAGCTTG GGTNGGTTTC ATAGGGTNCA	180
TTATGNACAC ATTGTTATTT TATCCCTTAA TNCTAGTAAA GAAATAGAAT CTGAAAATAA	240
GTAAAAC TAC TTGGAAAAAA NTTAAAAGAT ACAGAAATT CTATCTTAAA TGATGTGTGG	300
GCCNCTGTGA TTTTAGTNGG GNTGGTTAAA ANCCCAGAGG TGAAGAGNAT NCTCTATGCT	360
GTGNGGGGG	369

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCTCATCATG CTTCACGGGG GAGGCTGTGC GGGAAAGAATG CTCCCACACA GNATAAAGAA	60
TGCTCCCGCA CAGGATAGAG AATGCCCG CACAGCATAG AGAAGCCCCC GCACAGCATA	120
GAGAATGCC CCNCACAGCA TAGAGAAGCC CCCGCACAGC ATAGAGAATG CTCTTCACCT	180
CTGGGTTTT AACCAAGCAA ACTAAAATCA CAGAGGSCMA CACATCATT AAGATAGAAA	240
TTTCTGTATC TTTTAATTTC TTTCMAGTA GTTTTACTTA TTTTCAGATT CTATTTCTTT	300
ACTAGAATTA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACMAACMMAA	360
GCTAGGTTTT TTTCATAGST CTTCTTCAG ATTGAATGAA CGTCTGTTCT AAAATTTAAC	420

CCCCCAGGGA AATATTCACT TAACTATGTT AAAAACCCAG ACTTGTGATT GAGTTTGCC 480
TGAAAATGCT TTCATAATTA TGTGTGAATG TGTGTC 516

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GTATAATGCA GGTGCTATAA GGTGAGCATG AGACACAGAT CTTTGCTTTC CACCCCTGTTC 60
TTCTTATGGT TGGGTATTCT TGTCACAGTA ACTTAACTGA TCTAGGAAAG AAAAAATGTT 120
T 121

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

TGGAGACTGG AACACAAAC 18

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GTGTGGCCAG GGTAGAGAAC T 21

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATCTCCGGCA GGCATATCT

19

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGAAATCACA GCCAAGATGA G

21

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CCATAGCCTG TTTCGTAGC

19

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CCATAGCCTA TTTCGTAGC

19

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2791 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TGGGACAGGC	AGCTCCGGGG	TCCGCGGTTT	CACATCGGAA	ACAAAACAGC	GGCTGGTCTG	60
GAAGGAAACCT	GAGCTACGAG	CCGCAGGCGGC	AGCGGGGCAG	CGGGGAAGCG	TATACCTAAT	120
CTGGGAGCCT	GCAAGTGACA	ACAGCCTTG	CGGTCCCTAG	ACAGCTTGGC	CTGGAGGAGA	180
ACACATGAAA	GAAAGAACCT	CAAGAGGCTT	TGTTTCTGT	GAAACAGTAT	TTCTATACAG	240
TTGCTCCAAT	GACAGAGTTA	CCTGCACCGT	TGTCCCTACTT	CCAGAAATGCA	CAGATGTCTG	300
AGGACAACCA	CCTGAGCAAT	ACTGTACGTA	GCCAGAATGA	CAATAGAGAA	CGGCAGGAGC	360
ACAACGACAG	ACGGAGCCTT	GGCCACCCCTG	AGCCATTATC	TAATGGACGA	CCCCAGGGTA	420
ACTCCCGGCA	GGTGGTGGAG	CAAGATGAGG	AAGAAGATGA	GGAGCTGACA	TTGAAATATG	480
GCGCCAAGCA	TGTGATCATG	CTCTTTGTCC	CTGTGACTCT	CTGCATGGTG	GTGGTCGTGG	540
CTACCATTAA	GTCAGTCAGC	TTTATACCC	GGAAGGATGG	GCAGCTAATC	TATACCCAT	600
TCACAGAAGA	TACCGAGACT	GTGGGCCAGA	GAGCCCTGCA	CTCAATTCTG	AATGCTGCCA	660
TCATGATCAG	TGTCATTGTT	GTCATGACTA	TCCTCCTGGT	GGTTCTGTAT	AAATACAGGT	720
GCTATAAGGT	CATCCATGCC	TGGCTTATTA	TATCATCTCT	ATTGTTGCTG	TTCTTTTTT	780
CATTCAATTAA	CTTGGGGGAA	GTGTTAAAAA	CCTATAACGT	TGCTGTGGAC	TACATTACTG	840
TTGCACTCCT	GATCTGGAAT	TTTGGTGTGG	TGGGAATGAT	TTCCATTAC	TGGAAAGGTC	900
CACTTCGACT	CCAGCAGGCA	TATCTCATTA	TGATTAGTGC	CCTCATGGCC	CTGGTGTGTTA	960
TCAAGTACCT	CCCTGAATGG	ACTGCCTGGC	TCATCTTGGC	TGTGATTCA	GTATATGATT	1020
TAGTGGCTGT	TTTGTGTCCG	AAAGGTCCAC	TTCGTATGCT	GGTTGAAACA	GCTCAGGAGA	1080
GAAATGAAAC	GCTTTTCCA	GCTCTCATTT	ACTCCTAAC	AATGGTGTGG	TTGGTGAATA	1140
TGGCAGAAGG	AGACCCGGAA	GCTCAAAGGA	GAGTATCAA	AAATTCCAAG	TATAATGCAG	1200
AAAGCACAGA	AAGGGAGTCA	CAAGACACTG	TTGCAGAGAA	TGATGATGGC	GGGTTCACTG	1260
AGGAATGGGA	AGCCAGAGG	GACAGTCATC	TAGGGCCTCA	TCGCTCTACA	CCTGAGTCAC	1320
GAGCTGCTGT	CCAGGAACCTT	TCCAGCAGTA	TCCTCGCTGG	TGAAGACCCA	GAGGAAAGGG	1380
GAGTAAAAC	TGGATTGGGA	GATTCATTT	TCTACAGTGT	TCTGGTTGGT	AAAGCCTCAG	1440
CAACAGCCAG	TGGAGACTGG	AACACAAACCA	TAGCCTGTTT	CGTAGCCATA	TTAATTGGTT	1500
TGTGCCTTAC	ATTATTACTC	CTTGCATTT	TCAAGAAAGC	ATTGCCAGCT	CTTCCAATCT	1560
CCATCACCTT	TGGGCTTGTT	TTCTACTTTG	CCACAGATTA	TCTTGTACAG	CCTTTTATGG	1620
ACCAATTAGC	ATTCCATCAA	TTTATATCT	AGCATATTG	CGGTTAGAAT	CCCATGGATG	1680
TTTCTTCTTT	GACTATAACC	AAATCTGGGG	AGGACAAAGG	TGATTTCCCT	GTGTCCACAT	1740

CTAACAAAGT CAAGATTCCC GGCTGGACTT TTGCAGCTTC CTTCCAAGTC TTCTGACCA	1800
CCTTGCACTA TTGGACTTTG GAAGGAGGTG CCTATAGAAA ACGATTGAA ACATACTTCA	1860
TCGCAGTGGAA CTGTGTCCT CGGTGCAGAA ACTACCAGAT TTGAGGGACG AGGTCAAGGA	1920
GATATGATAG GCCCGGAAGT TGCTGTGCC CATCAGCAGC TTGACCGTG GTCACAGGAC	1980
GATTCACTG ACAC TGCGAA CTCTCAGGAC TACCGGTTAC CAAGAGGTTA GGTGAAGTGG	2040
TTTAAACCAA ACGGAACCTCT TCATCTTAAA CTACACGTTG AAAATCAACC CAATAATTCT	2100
GTATTAAC TG AATTCTGAAC TTTTCAGGAG GTACTGTGAG GAAGAGCAGG CACCAGCAGC	2160
AGAATGGGGA ATGGAGAGGT GGGCAGGGGT TCCAGCTTCC CTTTGATT TTGCTGCAGA	2220
CTCATCCTTT TTAAATGAGA CTTGTTTCC CCTCTCTTG AGTCAAGTCA AATATGTAGA	2280
TTGCCTTGG CAATTCTCT TCTCAAGCAC TGACACTCAT TACCGTCTGT GATTGCCATT	2340
TCTTCCAAG GCCAGTCTGA ACCTGAGGTT GCTTTATCCT AAAAGTTTA ACCTCAGGTT	2400
CCAAATTCAAG TAAATTTGG AAACAGTACA GCTATTCCTC ATCAATTCTC TATCATGTTG	2460
AAGTCAAATT TGGATTTCC ACCAAATTCT GAATTGTTAG ACATACTTGT ACGCTCACTT	2520
GCCCCCAGAT GCCTCCTCTG TCCTCATTCT TCTCTCCCAC ACAAGCAGTC TTTTCTACA	2580
GCCAGTAAGG CAGCTCTGTC TGGTAGCAGA TGGTCCCATT ATTCTAGGGT CTTACTCTT	2640
GTATGATGAA AAGAATGTGT TATGAATCGG TGCTGTCAGC CCTGCTGTCA GACCTTCTTC	2700
CACAGCAAAT GAGATGTATG CCCAAAGCGG TAGAATTAAA GAAGAGTAAA ATGGCTGTTG	2760
AAGCAAAAAA AAAAAAAA AAAAAAAA A	2791

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met			
1	5	10	15
Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn			
20	25	30	
Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu			
35	40	45	
Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu			
50	55	60	

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
 65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
 85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
 100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
 115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
 130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
 145 150 155 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Phe Phe
 165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
 180 185 190

Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
 195 200 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
 210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
 225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
 245 250 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
 260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
 275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
 290 295 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
 305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
 325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
 340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
 355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
 370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
 385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile

405

410

415

Gly	Leu	Cys	Leu	Thr	Leu	Leu	Leu	Ala	Ile	Phe	Lys	Lys	Ala	Leu	
420							425				430				
Pro	Ala	Leu	Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Val	Phe	Tyr	Phe	Ala
435							440				445				
Thr	Asp	Tyr	Leu	Val	Gln	Pro	Phe	Met	Asp	Gln	Leu	Ala	Phe	His	Gln
450						455				460					
Phe	Tyr	Ile													
465															

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1964 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACCANACANC	GGCAGCTGAG	GCGGAAACCT	AGGCTGCGAG	CCGGCCGCC	GGCGCGGGAG	60
AGAGAAGGAA	CCAACACAAG	ACAGCAGCCC	TTCGAGGTCT	TTAGGCAGCT	TGGAGGAGAA	120
CACATGAGAG	AAAGAATCCC	AAGAGGTTTT	GTGTTCTTG	AGAAGGTATT	TCTGTCCAGC	180
TGCTCCAATG	ACAGAGATAC	CTGCACCTTT	GTCTACTTC	CAGAATGCC	AGATGTCTGA	240
GGACAGCCAC	TCCAGCAGCG	CCATCCGGAG	CCAGAATGAC	AGCCAAGAAC	GGCAGCAGCA	300
GCATGACAGG	CAGAGACTTG	ACAACCCTGA	GCCAATATCT	AATGGCGGC	CCCAGAGTAA	360
CTCAAGACAG	GTGGTGGAAC	AAGATGAGGA	GGAAGACGAA	GAGCTGACAT	TGAAATATGG	420
AGCCAAGCAT	GTCATCATGC	TCTTGTC	CGTGACCC	TGCATGGTC	TCGTCGTGGC	480
CACCATCAAA	TCAGTCAGCT	TCTATACCCG	GAAGGACGGT	CAGCTAATCT	ACACCCATT	540
CACAGAAGAC	ACTGAGACTG	TAGGCCAAAG	AGCCCTGCAC	TCGATCCTGA	ATGCGGCCAT	600
CATGATCAGT	GTCATTGTCA	TTATGACCAT	CCTCCTGGTG	GTCCTGTATA	AATACAGGTG	660
CTACAAGGTC	ATCCACGCCT	GGCTTATTAT	TTCATCTCTG	TTGTTGCTGT	TCTTTTTTC	720
GTTCAATTAC	TTAGGGGAAG	TATTAAGAC	CTACAATGTC	GCCGTGGACT	ACGTTACAGT	780
AGCACTCCTA	ATCTGGAATT	TTGGTGTGGT	CGGGATGATT	GCCATCCACT	GGAAAGGCC	840
CCTTCGACTG	CAGCAGCGT	ATCTCATTAT	GATCAGTGCC	CTCATGGCCC	TGGTATTAT	900
CAAGTACCTC	CCCGAATGGA	CCGCATGGCT	CATCTTGGCT	GTGATTCAG	TATATGATT	960
GGTGGCTGTT	TTATGTCCA	AAGGCCACT	TCGTATGCTG	GTTGAAACAG	CTCAGGAAAG	1020
AAATGAGACT	CTCTTCCAG	CTCTTATCTA	TTCCCTAACAA	ATGGTGTGGT	TGGTGAATAT	1080

GGCTGAAGGA GACCCAGAAG CCCAAAGGAG GGTACCCAAG AACCCCAAGT ATAACACACA	1140
AAGAGCGGAG AGAGAGACAC AGGACAGTGG TTCTGGGAAC GATGATGGTG GCTTCAGTGA	1200
GGAGTGGGAG GCCCAAAGAG ACAGTCACCT GGGGCCTCAT CGCTCCACTC CCGAGTCAAG	1260
AGCTGCTGTC CAGGAACCTT CTGGGAGCAT TCTAACGAGT GAAGACCCGG AGGAAAGAGG	1320
AGTAAAACCTT GGACTGGGAG ATTCATTTT CTACAGTGT CTGGTTGGTA AGGCCTCAGC	1380
AACCGCCAGT GGAGACTGGA ACACAACCAT AGCCTGCTT GTAGCCATAC TGATCGGCCT	1440
GTGCCTTACA TTACTCCTGC TCGCCATTTT CAAGAAAGCG TTGCCAGCCC TCCCCATCTC	1500
CATCACCTTC GGGCTCGTGT TCTACTTCGC CACGGATTAC CTTGTGCAGC CCTTCATGGA	1560
CCAACATTGCA TTCCATCAGT TTTATATCTA GCCTTCTGC AGTTAGAACAA TGGATGTTTC	1620
TTCTTGATT ATCAAAAACA CAAAAACAGA GAGCAAGCCC GAGGAGGAGA CTGGTGACTT	1680
TCCTGTGTCC TCAGCTAACAA AAGGCAGGAC TCCAGCTGGA CTTCTGCAGC TTCCCTCCGA	1740
GTCTCCCTAG CCACCCGCAC TACTGGACTG TGGAAGGAAG CGTCTACAGA GGAACGGTTT	1800
CCAACATCCA TCGCTGCAGC AGACGGTGTG CCTCAGTGAC TTGAGAGACA AGGACAAGGA	1860
AATGTGCTGG GCCAAGGAGC TGCCGTGCTC TGCTAGCTT GACC GTGGGC ATGGAGATT	1920
ACCCGCACTG TGAACCTCT AAGGTAAACA AAGTGAGGTG AAC	1964

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCTGGCA CGAGGGCATT TCCAGCAGTG AGGAGACAGC CAGAACAAAG CTTTGAGC	60
TGAAGGAACC TGAGACAGAA GCTAGTCCCC CCTCTGAATT TTACTGATGA AGAAACTGAG	120
GCCACAGAGC TAAAGTGACT TTTCCAAGG TCGCCAGCG AGGACGTGGG ACTTCTCAGA	180
CGTCAGGAGA GTGATGTGAG GGAGCTGTGT GACCATAGAA AGTGACGTGT TAAAAACCAAG	240
CGCTGCCCTC TTTGAAAGCC AGGGAGCATC ATTCAATTAG CCTGCTGAGA AGAAGAAACC	300
AAGTGTCCGG GATTCAAGAC CTCTCTGCGG CCCAAAGTGT TCGTGGTGCT TCCAGAGGCA	360
GGGCTATGCT CACATTCTGAC GCGAGGAAGA AGTGTGTGAT GAGCGGACGT	420
CCCTAATGTC GGCGAGAGC CCCACGCCGC GCTCTGCCA GGAGGGCAGG CAGGGCCAG	480
AGGATGGAGA GAATACTGCC CAGTGGAGAA GCCAGGAGAA CGAGGAGGAC GGTGAGGAGG	540

ACCCCTGACCG CTATGTCTGT AGTGGGGTTC CGGGCGGCC GCCAGGCCTG GAGGAAGAGC	600
TGACCCCTCAA ATACGGAGCG AAGCATGTGA TCATGCTGTT TGTGCCTGTC ACTCTGTGCA	660
TGATCGTGGT GGTAGCCACC ATCAAGTCTG TGCCTTCTA CACAGAGAAG AATGGACAGC	720
TCATCTACAC GCCATTCACT GAGGACACAC CCTCGGTGGG CCAGGCCTC CTCAACTCCG	780
TGCTGAACAC CCTCATCATG ATCAGCGTCA TCGTGGTTAT GACCATCTTC TTGGTGGTGC	840
TCTACAAGTA CCGCTGCTAC AAGTCATCC ATGGCTGGTT GATCATGTCT TCACTGATGC	900
TGCTGTTCCCT CTTCACCTAT ATCTACCTTG GGGAAAGTGCT CAAGACCTAC AATGTGGCCA	960
TGGACTACCC CACCCCTTTG CTGACTGTCT GGAACCTCGG GGCAGTGGGC ATGGTGTGCA	1020
TCCACTGGAA GGGCCCTCTG GTGCTGCAGC AGGCCTACCT CATCATGATC AGTGCCTCA	1080
TGGCCCTAGT GTTCATCAAG TACCTCCAG AGTGGTCCGC GTGGGTCACTC CTGGGCGCCA	1140
TCTCTGTGTA TGATCTCGTG GCTGTGCTGT GTCCCAAAGG GCCTCTGAGA ATGCTGGTAG	1200
AAACTGCCCA GGAGAGAAAT GAGCCCATAT TCCCTGCCCT GATATACTCA TCTGCCATGG	1260
TGTGGACGGT TGGCATGGCG AAGCTGGACC CCTCCTCTCA GGGTGCCCTC CAGCTCCCT	1320
ACGACCCGGA GATGGAAGAA GACTCCTATG ACAGTTTGG GGAGCCTCA TACCCCGAAG	1380
TCTTGAGCC TCCCTTGACT GGCTACCCAG GGGAGGAGCT GGAGGAAGAG GAGGAAAGGG	1440
CGGTGAAGCT TGGCCTCGGG GACTTCATCT TCTACAGTGT GCTGGTGGGC AAGGCGGCTG	1500
CCACGGGCAG CGGGGACTGG AATACCACGC TGGCCTGCTT CGTGGCCATC CTCATTGGCT	1560
TGTGTCTGAC CCTCCTGCTG CTTGCTGTGT TCAAGAAGGC GCTGCCGCC CTCCCCATCT	1620
CCATCACGTT CGGGCTCATC TTTTACTTCT CCACGGACAA CCTGGTGCAG CCGTTCATGG	1680
ACACCCCTGGC CTCCCATCAG CTCTACATCT GAGGGACATG GTGTGCCACA GGCTGCAAGC	1740
TGCAGGGAAT TTTCATTGGA TGCAGTTGTA TAGTTTACA CTCTAGTGCC ATATATTTT	1800
AAGACTTTTC TTTCCTTAAA AAATAAAGTA CGTGTAACT TGTTGAGGAG GAGGCAGAAC	1860
CAGCTTTG GTGCCAGCTG TTTCATCACC AGACTTTGGC TCCCGCTTG GGGAGCGCCT	1920
CGCTTCACGG ACAGGAAGCA CAGCAGGTTT ATCCAGATGA ACTGAGAAGG TCAGATTAGG	1980
GTGGGGAGAA GAGCATCCGG CATGAGGGCT GAGATGCCA AAGAGTGTGC TCGGGAGTGG	2040
CCCCTGGCAC CTGGGTGCTC TGGCTGGAGA GGAAAAGCCA GTTCCCTACG AGGAGTGTTC	2100
CCAATGCTTT GTCCATGATG TCCTTGTAT TTTATTNCCY TTANAAACTG ANTCCTNTTN	2160
TTNTTDCGGC AGTCACMCTN CTGGGRAGTG GCTTAATAGT AANATCAATA AANAGNTGAG	2220
TCCTNTTACA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	2280
AAAAAA	2285

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 448 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

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Met Leu Thr Phe Met Ala Ser Asp Ser Glu Glu Glu Val Cys Asp Glu
1           5           10           15

Arg Thr Ser Leu Met Ser Ala Glu Ser Pro Thr Pro Arg Ser Cys Gln
20          25           30

Glu Gly Arg Gln Gly Pro Glu Asp Gly Glu Asn Thr Ala Gln Trp Arg
35          40           45

Ser Gln Glu Asn Glu Glu Asp Gly Glu Asp Pro Asp Arg Tyr Val
50          55           60

Cys Ser Gly Val Pro Gly Arg Pro Pro Gly Leu Glu Glu Glu Leu Thr
65          70           75           80

Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr
85          90           95

Leu Cys Met Ile Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr
100         105          110

Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr
115         120          125

Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile
130         135          140

Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu Val Val Leu Tyr
145         150          155          160

Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser
165         170          175

Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Leu
180         185          190

Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Leu Thr Val
195         200          205

Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His Trp Lys Gly Pro
210         215          220

Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala
225         230          235          240

Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu
245         250          255

Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly
260         265          270

Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile
275         280          285

Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met
290         295          300

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Ala	Lys	Leu	Asp	Pro	Ser	Ser	Gln	Gly	Ala	Leu	Gln	Leu	Pro	Tyr	Asp
305															320
Pro	Glu	Met	Glu	Glu	Asp	Ser	Tyr	Asp	Ser	Phe	Gly	Glu	Pro	Ser	Tyr
	325									330					335
Pro	Glu	Val	Phe	Glu	Pro	Pro	Leu	Thr	Gly	Tyr	Pro	Gly	Glu	Glu	Leu
		340						345							350
Glu	Glu	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly	Asp	Phe	Ile	
				355			360				365				
Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ala	Ala	Thr	Gly	Ser	Gly	Asp
				370			375				380				
Trp	Asn	Thr	Thr	Leu	Ala	Cys	Phe	Val	Ala	Ile	Leu	Ile	Gly	Leu	Cys
					390					395					400
Leu	Thr	Leu	Leu	Leu	Leu	Ala	Val	Phe	Lys	Lys	Ala	Leu	Pro	Ala	Leu
							405		410					415	
Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Ile	Phe	Tyr	Phe	Ser	Thr	Asp	Asn
					420			425				430			
Leu	Val	Arg	Pro	Phe	Met	Asp	Thr	Leu	Ala	Ser	His	Gln	Leu	Tyr	Ile
					435			440				445			

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys	His	Val	Ile	Met	Leu	Phe
1				5					10					15	
Val	Pro	Val	Thr	Leu	Cys	Met	Ile	Val	Val	Val	Ala	Thr	Ile	Lys	Ser
					20			25					30		
Val	Arg	Phe	Tyr	Thr	Glu	Lys	Asn	Gly	Gln	Leu	Ile	Tyr	Thr	Pro	Phe
					35			40				45			
Thr	Glu	Asp	Thr	Pro	Ser	Val	Gly	Gln	Arg	Leu	Leu	Asn	Ser	Val	Leu
					50			55				60			
Asn	Thr	Leu	Ile	Met	Ile	Ser	Val	Ile	Val	Val	Met	Thr	Ile	Phe	Leu
					65			70			75			80	
Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys	Phe	Ile	His	Gly	Trp	Leu
					85			90				95			
Ile	Met	Ser	Ser	Leu	Met	Leu	Leu	Phe	Leu	Phe	Thr	Tyr	Ile	Tyr	Leu
					100			105				110			
Gly	Glu	Val	Leu	Lys	Thr	Tyr	Asn	Val	Ala	Met	Asp	Tyr	Pro	Thr	Leu
					115			120				125			

Leu Leu Thr Val Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His
 130 135 140
 Trp Lys Gly Pro Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser
 145 150 155 160
 Ala Leu Met Ala Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala
 165 170 175
 Trp Val Ile Leu Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu
 180 185 190
 Cys Pro Lys Gly Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg
 195 200 205
 Asn Glu Pro Ile Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp
 210 215 220
 Thr Val Gly Met Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln
 225 230 235 240
 Leu Pro Tyr Asp Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly
 245 250 255
 Glu Pro Ser Tyr Pro Glu Val Phe Glu Pro Pro Leu Thr Gly Tyr Pro
 260 265 270
 Gly Glu Glu Leu Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu
 275 280 285
 Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr
 290 295 300
 Gly Ser Gly Asp Trp Asn Thr Thr Leu Ala Cys Phe Val Ala Ile Leu
 305 310 315 320
 Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Val Phe Lys Lys Ala
 325 330 335
 Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe
 340 345 350
 Ser Thr Asp Asn Leu Val Arg Pro Phe Met Asp Thr Leu Ala Ser His
 355 360 365
 Gln Leu Tyr Ile
 370

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGTACCGCCA CCATGACAGA GGTACCTGCA C

31

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAATTCACTG GCTGTAGAAA AAGAC

25

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGATCCGGTC CACTTCGTAT GCTG

24

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTTTTTGAAT TCTTAGGCTA TGGTTGTGTT CCA

33

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GATTAGTGGT TGTTTTGTG

19

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GATTAGTGGC TGTTTTGTG

19

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TTTTTCCAGC TCTCATTAA

19

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

TTTTTCCAGT TCTCATTAA

19

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TACAGTGTTC TGGTTGGTA

19

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TACAGTGTTC TGGTTGGTA

19

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TACAGTGTG TGGTTGGTA

19

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1092 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GTCTAGATAA GNCAACATTC AGGGGTAGAA GGGGACTGTT TATTTTTCC TTTAGTCTCT	60
CTTAAAGAGT GAGAAAATT TTCCCAGGAA TCCCGGTGGA CTTTGCTTCA CCACTCATAG	120
GTTCATACCA AGTTACAACC CCACAACCTT AGAGCTTTG TTAGGAAGAG GCTTGGTGG	180
ATTACCGTGC TTGGCTTGGC TTGGTCAGGA TTCACCACCA GAGTCATGTG GGAGGGGGTG	240
GGAACCCAAA CAATTCAAGGA TTCTGCCCTC AGGAAATAAA GGAGAAAATA GCTGTTGGAT	300
AAACTACCAG CAGGCACACTGC TACAGCCCAT GCTTGTTGGT TTAAGGGCCA GCTAGTTACA	360
ATGACAGCTA GTTACTGTTT CCATGTAATT TTCTTAAAGG TATTAAATTT TTCTAAATAT	420
TAGAGCTGTA ACTTCCACTT TCTCTTGAAG GCACAGWAAG GGAGTCACAA GACACTGTTG	480
CAGAGAATGA TGATGGCGGG TTCAGTGAGG AATGGGAASC CCAGRGGGAC ANTCACTAG	540
GGCCTCATCG CTCTACACCT GAGTCACGAG CTKCTNTCCA GGRACHTTCC ANCAGTATCC	600
TCGCTGGTGA AGACCCAGAG GAAAGNATGT TCANTTCTCC ATNTTCAAA GTCATGGATT	660
CCTTGTAGTA GCTACATTAT CAACCTTTT GAGAATAAAA TGAATTGAGA GTGTTACAGT	720
CTAATTCTAT ATCACATGTA ACTTTTATTT GGATATATCA GTAATAGTGC TTTTYNTTT	780
TTTTTTTTT TTTTTTTTT TTTTNGGNGA NAGAGTCTCG CTCTGTCGCC AGGTTGGAGT	840
GCAATGGTGC GATCTTGGCT CACTGAAAGC TCCACCNCCC GGGTTCAAGT GATTCTCCTG	900
CCTCAGCCNC CCAAGTAGNT GGGACTACAG GGGTGCGCCA CCACGCCTGG GATAATTTG	960
GGNTTTTTAG TAGAGATGGC GTTTCACCAN CTTGGNGCAG GCTGGTCTTG GAACTCCTGA	1020
NATCATGATC TGCCTGCCTT AGCCTCCCCA AAGTGCTGGG ATTNCAGGGG TGAGCCACTG	1080
TTCCCTGGGCC TC	1092

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CTGCAGTGAG CCGAGATCAT GCTGCTGTAC TCCAGCCTGG GCCACAGAGC CAAACTCCAT	60
CTCCCCAAAA AAAAAAAATAT TAATTAATAT GATNAAATGA TGCCTATCTC AGAATTCTTG	120
TAAGGATTTC TTAGKACAAG TGCTGGGTAT AAACATATANA TTCACTAGAT GNCGATTATT	180
ACTTAYTATT GTTATTGATA AATAACAGCA GCATCTACAG TTAAGACTCC AGAGTCAGTC	240
ACATAGAAC TGGNACTCCT ATTGTAGNAA ACCCCNMMAG AAAGAAAACA CAGCTGAAGC	300
CTAATTTGT ATATCATTAA CTGACTTCTC TCATTCAATTG TGGGGTTGAG TAGGGCAGTG	360
ATATTTTGA ATTGTGAAAT CATANCAAAG AGTGACCAAC TTTTTAATAT TTGTAACCTT	420

TCCTTTTAG GGGGAGTAAA ACTTGGATTG GGAGATTCA TTTTCTACAG TGTTCTGGTT	480
GGTAAAGCCT CAGCAACAGC CAGTGGAGAC TGGAACACAA CCATAGCCTG TTTCGTAGCC	540
ATATTAATTG TMMSTATACA CTAATAAGAA TGTGTCAGAG CTCTTAATGT CMAAACTTG	600
ATTACACAGT CCCTTTAAGG CAGTTCTGTT TTAACCCCAG GTGGGTTAAA TATTCCAGCT	660
ATCTGAGGAG CTTTNGATA ATTGGACCTC ACCTTAGTAG TTCTCTACCC TGGCCACACA	720
TTAGAATCAC TTGGGAGCTT TTAAAACGT AAGCTCTGCC CTGAGATATT CTTACTCAAT	780
TTAATTGTGT AGTTTTAAA ATTCCCCAGG AAATTCTGGT ATTTCTGTTT AGGAACCGCT	840
GCCTCAAGCC TAGCAGCACA GATATGTAGG AAATTAGCTC TGTAAGGTTG GTCTTACAGG	900
GATAAACAGA TCCTTCCTTA GTCCCTGGAC TTAATCACTG AGAGTTGGG TGGTGGTTT	960
GGATTTAATG ACACAACCTG TAGCATGCAG TGTTACTTAA GAC	1003

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1726 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGATCCCTCC CCTTTTTAGA CCATACAAGG TAACTTCCGG ACgttGCCAT GGCATCTGTA	60
AACTGTCATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA	120
TAGTGAGCAG TGAGGATAAC CAGAGGTCAC TCTCCTCACC ATCTTGGTTT TGGTGGGTTT	180
TGGCCAGCTT CTTTATTGCA ACCAGTTTA TCAGCAAGAT CTTTATGAGC TGTATCTTGT	240
GCTGACTTCC TATCTCATCC CGNAACTAAG AGTACCTAAC CTCCTGCAA TTGMAGNCCA	300
GNAGGTCTTG GNCTTATTN ACCCAGCCCC TATTCAARAT AGAGTNGYTC TTGGNCCAAA	360
CGCCYCTGAC ACAAGGATT TAAAGTCTTA TTAATTAAGG TAAGATAGKT CCTTGSATAT	420
GTGGTCTGAA ATCACAGAAA GCTGAATTG GAAAAAGGTG CTTGGASCTG CAGCCAGTAA	480
ACAAGTTTC ATGCAGGTGT CAGTATTAA GGTACATCTC AAAGGATAAG TACAATTGTG	540
TATGTTGGGA TGAACAGAGA GAATGGAGCA ANCCAAGACC CAGGTAAAAG AGAGGACCTG	600
AATGCCTTCA GTGAACAATG ATAGATAATC TAGACTTTA AACTGCATAC TTCCTGTACA	660
TTGTTTTTC TTGCTTCAGG TTTTTAGAAC TCATAGTGAC GGGTCTGTTG TTAATCCCAG	720
GTCTAACCGT TACCTTGATT CTGCTGAGAA TCTGATTAC TGAAAATGTT TTTCTTGTC	780
TTATAGAATG ACAATAGAGA ACGGCAGGAG CACAACGACA GACGGAGCCT TGGCCACCCT	840

GANCCATTAT CTAATGGACG ACCCAGGGTA ACTCCCGCA GGTGGTGGAN CAAGATGAGG	900
AAGAAAGATGA GGANCTGACA TTGAAATATG NCGSCAAGCA TGTGATCATG CTCTTGKCC	960
CTGTGACTCT CTGCATGGTG GTGGTCGTGG NTACCATTAA GTCAGTCAGC TTTTATAACCC	1020
GGAAGGATGG GCAGCTGTAC GTATGAGTTT KGTTTTATTA TTCTCAAASC CAGTGTGGCT	1080
TTTCTTACA GCATGTCATC ATCACCTGA AGGCCTCTNC ATTGAAGGGG CATGACTTAG	1140
CTGGAGAGCC CATCCTCTGT GATGGTCAGG AGCAGTTGAG AGANCGAGGG GTTATTACTT	1200
CATGTTTAA GTGGAGAAAA GGAACACTGC AGAAGTATGT TTCCTGTATG GTATTACTGG	1260
ATAGGGCTGA AGTTATGCTG AATTGAACAC ATAAATTCTT TTCCACCTCA GGGNCATTGG	1320
GCGCCCATTG NTCTTCTGCC TAGAATATTC TTTCCCTTNC TNACTTKGGN GGATTAAATT	1380
CCTGTATCC CCCTCCTCTT GGTGTTATAT ATAAAGTNTT GGTGCCGCAA AAGAAGTAGC	1440
ACTCGAATAT AAAATTTCC TTTTAATTCT CAGCAAGGNA AGTTACTTCT ATATAGAAGG	1500
GTGCACCCNT ACAGATGGAA CAATGGCAAG CGCACATTG GGACAAGGG GGGGAAAGGG	1560
TTCTTATCCC TGACACACGT GGTCCNGCT GNTGTGTNCT NCCCCACTG ANTAGGGTTA	1620
GACTGGACAG GCTTAAACTA ATTCCAATTG GNTAATTAA AGAGAATNAT GGGGTGAATG	1680
CTTGGGAGG AGTCAAGGAA GAGNAGGTAG NAGGTAACCTT GAATGA	1726

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CNCGTATAAA AGACCAACAT TGCCANCNAC AACCAACAGGC AAGATCTTCT CCTACCTTCC	60
CCCNNGGTGT AATACCAAGT ATTNCNAAT TTGTGATAAA CTTTCATTGG AAAGTGACCA	120
CCCTCCTTGG TTAATACATT GTCTGTGCCT GCTTCACAC TACAGTAGCA CAGTTGAGTG	180
TTTGCCTGG AGACCATATG ACCCATAGAG CTTAAATAT TCAGTCTGGC TTTTACAGA	240
GATGTTCTG ACTTTGTTAA TAGAAAATCA ACCCAACTGG TTTAAATAAT GCACATACTT	300
TCTCTCTCAT AGAGTAGTGC AGAGGTAGNC AGTCCAGATT AGTASGGTGG CTTCACGTT	360
ATCCAAGGAC TCAATCTCCT TCTTTCTCT TTAGCTTCTA ACCTCTAGCT TACTTCAGGG	420
TCCAGGCTGG AGCCCTASCC TTCATTCTG ACAGTAGGAA GGAGTAGGGG AGAAAAGAAC	480
ATAGGACATG TCAGCAGAAT TCTCTCCTTA GAAGTTCCAT ACACAACACA TCTCCCTAGA	540
AGTCATTGCC CTTACTTGTT CTCATAGCCA TCCTAAATAT AAGGGAGTCA GAAGTAAAGT	600

CTKKNTGGCT	GGGAATATTG	GCACCTGGAA	AAAAAATGTT	TTTCTGTGAA	TGAGAAACAA	660		
GGGGAAAGATG	GATATGTGAC	ATTATCTTAA	GACAACTCCA	GTTGCAATT	CTCTGCAGAT	720		
GAGAGGCACT	AATTATAAGC	CATATTACCT	TTCTTCTGAC	AACCACTTGT	CAGCCCNCGT	780		
GGTTTCTGTG	GCAGAATCTG	GTTCYATAMC	AAGTTCCCTAA	TAANCTGTAS	CCNAAAAAAT	840		
TTGATGAGGT	ATTATAATTA	TTTCAATATA	AAGCACCCAC	TAGATGGAGC	CAGTGTCTGC	900		
TTCACATGTT	AAGTCCTTCT	TTCCATATGT	TAGACATT	CTTTGAAGCA	ATTTTAGAGT	960		
GTAGCTGTTT	TTCTCAGGTT	AAAAATTCTT	AGCTAGGATT	GGTGAGTTGG	GGAAAAGTGA	1020		
CTTATAAGAT	NCGAATTGAA	TTAAGAAAAA	GAAAATTCTG	TGTTGGAGGT	GGTAATGTGG	1080		
KTGGTGATCT	YCATTAACAC	TGANCTAGGG	CTTKGKGTT	TGKTTTATTG	TAGAATCTAT	1140		
ACCCCATTCA	NAGAAGATAC	CGAGACTGTG	GGCCAGAGAG	CCCTGCAC	TCAATTCTGAAT	1200		
GCTGCCATCA	TGATCAGNGT	CATTGTWGTC	ATGACTANN	TCCTGGTGGT	TCWGTATAAA	1260		
TACAGGTGCT	ATAAGGTGAG	CATGAGACAC	AGATCTTGN	TTTCCACCC	GTTCTTCTTA	1320		
TGGTTGGGTA	TTCTTGTAC	AGTAACCTAA	CTGATCTAGG	AAAGAAAAAA	TGTTTTGTCT	1380		
TCTAGAGATA	AGTTAATT	TAGTTTCTT	CCTCCTCACT	GTGGAACATT	CAAAAAATAC	1440		
AAAAAGGAAG	CCAGGTGCAT	GTGTAATGCC	AGGCTCAGAG	GCTGAGGCAG	GAGGATCGCT	1500		
TGGGCCAGG	AGTTCACAA	CAGCTTGGC	AACGTAGCAA	GACCCTGC	CTATTAAAGA	1560		
AAACAAAAAA	CAAATATTGG	AAGTATT	TATGCATGGA	ATCTATATGT	CATGAAAAAA	1620		
TTAGTGTAAA	ATATATATAT	TATGATTAGN	TATCAAGATT	TAGTGATAAT	TTATGTTATT	1680		
TTGGGATTT	AATGCC	TTT	TAGGCCATTG	TCTCAAMAAA	TAAAGCAGA	AAACAAAAAA	1740	
AGTTGTA	ACT	AAAAAATAAA	CATTCCATA	TAATAGCACA	ATCTAAGTGG	GTTTTGNTT	1800	
GTTTGT	TTG	TTG	AGGC	CCTGC	CCTNYCACCC	AGGNTGGAGT	GAAGTGCAGT	1860
GGCACGATT	TGG	CTCA	TG	CAG				1883

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1990 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGTTTGACA	ATTTCTCCGT	TCCACCC	TTG	ATTA	AAGT	TATTCA	TTTTTTAAGT	60
TTTAGCT	TTT	GG	ATATATGT	GTAAGTGTGG	TATGCTGTCT	AATGAATTAA	GACAATTGGT	120

NCTKTCTTTA	CCCMACANCT	GGACMAAGAG	CAGGCAAGAT	NCAANAATCA	AGTGACCCAG	180
NCAAACCAGA	CACATTTCT	GCTCTCAGCT	AGCTTGCCAC	CTAGAAAGAC	TGGTTGTCNA	240
AGTTGGAGTC	CAAGAATCGC	GGAGGATGTT	TAAAATGCAG	TTTCTCAGGT	TCTCNCCACC	300
CACCAGAAGT	TTTGATTCAT	TGAGTGGTGG	GAGAGGGCAG	AGATATTGC	GATTTAACAA	360
GCATTCTCTT	GATTGTGATG	CAGCTGGTTC	SCAAATAGGT	ACCCCTAAAGA	AATGACAGGT	420
GTAAATTTA	GGATGGCCAT	CGCTTGTATG	CCGGGAGAAG	CACACGCTGG	GCCCAATTAA	480
TATAGGGGCT	TTCGTCCTCA	GCTCGAGCAR	CCTCAGAACCC	CCGACAACCCY	ACGCCAGCKC	540
TCTGGGCGGA	TTCCRTCAAGK	TGGGGAAAGSC	CAGGTGGAGC	TCTGGKTTCT	CCCCGCAATC	600
GTTTCTCCAG	GCCGGAGGCC	CCGCCCCCTT	CCTCCTGGCT	CCTCCCTCC	TCCGTGGGCC	660
GNCCGCCAAC	GACGCCAGAG	CCGGAAATGA	CGACAACGGT	GAGGGTTCTC	GGCGGGGCC	720
TGGGACAGGC	AGCTCCGGGG	TCCNCGNNT	NACATCGGAA	ACAAAACAGC	GGCTGGTCTG	780
GAAGGAACCT	GAKCTACGAC	CCGCAGGCC	AGCGGGGCGG	CGGGGAAGCG	TATGTGCGTG	840
ATGGGGAGTC	CGGGCAAGCC	AGGAAGGCAC	CGCGGACATG	GGCGGCCGCG	GGCAGGGNCC	900
GGNCCTTTGT	GGCCGCCCGG	GCCGCGAAGC	CGGTGTCTA	AAAGATGAGG	GGCGGGCGC	960
GGCCGGTTGG	GGCTGGGAA	CCCCGTGTGG	GAAACCAGGA	GGGGCGGCC	GTTCCTCGGG	1020
CTTCGGGCGC	GGCCGGGTGG	AGAGAGATTC	CGGGGAGCCT	TGGTCCGGAA	ATGCTGTTTG	1080
CTCGAAGACG	TCTCAGGGCG	CAGGTGCCTT	GGGCCGGGAT	TAGTAGCCGT	CTGAACCTGGA	1140
GTGGAGTAGG	AGAAAGAGGA	AGCGTCTTGG	GCTGGGTCTG	CTTGAGCAAC	TGGTGAAACT	1200
CCGCGCCTCA	CGCCCCGGGT	GTGTCCTTGT	CCAGGGCGA	CGAGCATTCT	GGCGAAGTC	1260
CGCACGCCTC	TTGTTCGAGG	CGGAAGACGG	GGTCTTGATG	CTTCTCCTT	GGTCGGGACT	1320
GTCTCGAGGC	ATGCATGTCC	AGTGAECTTT	GTGTTGCTG	CTGCTTCCCT	CTCAGATTCT	1380
TCTCACCGTT	GTGGTCAGCT	CTGCTTTAGG	CATATTAATC	CATAGTGGAG	GCTGGGATGG	1440
GTGAGAGAAT	TGAGGTGACT	TTTCCATAAT	TCAGGTGAGA	TGTGATTAGA	GTYCGGATCC	1500
TNCGGTGGTG	GCAGAGGCTT	ACCAAGAAC	ACTAACGGGA	CATGGGAACC	AATTGAGGAT	1560
CCAGGGAAATA	AAAGTGTGAAG	TTGACTAGGA	GGTTTCAGT	TTAAGAACAT	GGCAGAGACA	1620
TTCTCAGAAA	TAAGGAAGTT	AGGAAGAAAG	ACCTGGTTA	GAGAGGAGGG	CGAGGAAGTG	1680
GTTTGGAAAGT	GTCACCTTGG	AAAGTGCAGC	AGGTGAAAAT	GCCCTGTGAA	CAGGACTGGA	1740
GCTGAAAACA	GGAATCAATT	CCATAGATTT	CCAGTTGATG	TTGGAGCAGT	GGAGAAGTCT	1800
AANCTAAGGA	AGGGGAAGAG	GAGGCCAAGC	CAAACACTTA	GGAACACTTN	CNACGAGGGG	1860
GTGGAAGAAG	AGCAAGGAGC	CAGCTGAGGA	GAATGAGTGT	GGTTGGAGAA	CCACCACAGC	1920
NCAGGGTCGC	CAGANCTGAG	GAAGGGGAGG	GAAGCTTATC	GAGKAMSGWC	RACMKCGAGT	1980
TGGCAGGGAT						1990

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTCTTTCCA TCTTCTCAC AGAGTTGTG CCTTACATTA TTACTCCTG CCATTTCAA	60
GAAAGCATTG TCAGCTCTC CAATCTCCAT CACCTTGGA CTTGTTTCT ACTTTGCCAC	120
AGATTATCTT GTACAGCCTT TTATGGACCA ATTAGCATT CATCAATTAT ATATCTAGCA	180
TATTTGCGGT TAGAATCCA TGGATGTTTC TTCTTGACT ATAACAAAAT CTGGGGAGGA	240
CAAAGGTGAT TTCCTGTGTC CACATCTAAC AAATCAAGAT CCCCAGCTGG ACTTTGGAG	300
GTTCCTTCCA AGTCTTCCTG ACCACCTTGC ACTATTGGAC TTTGGAAGGA GGTGCCTATA	360
GAAAACGATT TTGAACATAC TTCATCGCAG TGGACTGTGT CCTCGGTGCA GAAACTACCA	420
GATTTGAGGG ACGAGGTCAA GGAGATATGA TAGGCCCGGA AGTTGCTGTG CCCCACAGC	480
AGCTTGACGC GTGGTCACAG GACGATTTC ACTGACACTG CGAACTCTCA GGACTACCGT	540
TACCAAGAGG TTAGGTGAAG TGGTTAAC CAAACGGAAC TCTTCATCTT AAACATACACG	600
TTGAAAATCA ACCCAATAAT TCTGTATTAA CTGAATTCTG AACTTTCAAG GAGGTACTGT	660
GAGGAAGAGC AGGCACCAACC AGCAGAATGG GGAATGGAGA GGTGGGCAGG GGTTCCAGCT	720
TCCCTTTGAT TTTTG	736

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGATCCGCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTNNWGTAA AATAAGNATG TTATCTGNCC NNCCTGCCTT	180
GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC	240

AAATGATTT ATGAAAATAT AAAGATTAGN TTGAGTTGG GCCAGCATAG AAAAAGGAAT	300
GTTGAGAAC A TTCCNTTAAG GATTACTCAA GCYCCCCTT TGSTGKNWAA TCAGANNGTC	360
ATNNAMNTAT CNTNTGTGGG YTGAAAATGT TTGGTTGTCT CAGGCGGTTC CTACTTATTG	420
CTAAAGAGTC CTACCTTGAG CTTATAGTAA ATTTGTCAGT TAGTTGAAAG TCGTGACAAA	480
TTAATACATT CCTGGTTAC AAATTGGTCT TATAAGTATT TGATTGGTNT AAATGNATT	540
ACTAGGATT AACTAACAAAT GGATGACCTG GTGAAATCCT ATTTCAGACC TAATCTGGGA	600
GCCTGCAAGT GACAACAGCC TTTGCGGTCC TTAGACAGCT TGGCCTGGAG GAGAACACAT	660
GAAAGAMMGG TTTGWNTCTG NTTAWTGTAA TCTATGRAAG TGTTTTWAT MACAGTATAA	720
TTGTMTGMAC AAAGTTCTGT TTTTCTTCC CTTNCAGAA CCTCAAGAGG CTTTGTTC	780
TGTGAAACAG TATTCTATA CAGNTGCTCC AATGACAGAG TNACCTGCAC CGTTGTCCTA	840
CTTCCAGAAT GCACAGATGT CTGAGGACAA CCACCTGAGC AATACTGTAC GTAGCCAGGT	900
ACAGCGTCAG TYTCTNAAAC TGCCTYYGNC AGACTGGATT CACTTATCAT CTCCCCCTCAC	960
CTCTGAGAAA TGCTGAGGGG GSTAGGNAGG GCTTTCTCTA CTTNACCACA TTTNATAATT	1020
ATTTTGGGT GACCTTCAGC TGATCGCTGG GAGGGACACA GGGCTTNTTT AACACATAGG	1080
GTGTTGGATA CAGNCCCTCC CTAATTACA TTTCANC	1117

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CTGCAGCTTT CCTTTAAACT AGGAAGACTT GTTCCTATAC CCCAGTAACG ATACACTGTA	60
CACTAAGCAA ATAGCAGTCA AACCCAAATG AAATTTNTAC AGATGTTCTG TGTCATTAA	120
TNTTGTAACT GTTGTCTCCC CCACCCCCAC CAGTTCACCT GCCATTATT TCATATTCA	180
TCAACGTCTN NNTGTGTAAA AAGAGACAAA AAACATTAAA CTTTTTCCT TCGTTAATC	240
CTCCCTACCA CCCATTACA AGTTAGCCC ATACATTAA TTAGATGTCT TTTATGTTT	300
TCTTTNCTA GATTTAGTGG CTGTTNGTG TCCGAAAGGT CCACCTCGTA TGCTGGTTGA	360
AACAGCTCAG GAGAGAAATG AAACGCTTT TCCAGCTCTC ATTTACTCCT GTAAGTATT	420
GGAGAATGAT ATTGAATTAG TAATCAGNGT AGAATTATC GGGAACTTGA AGANATGTNA	480
CTATGGCAAT TTCANGGNAC TTGTCTCATC TTAAATGANA GNATCCCTGG ACTCCTGNAG	540

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CCCCGTCNAT	GCATACTTTG	TGTGTCCAGT	GCTTACCTGG	AATCCNGTCT	TTCCCAACAG	60
CAACAATGGT	GTGGTTGGTG	AATATGGCAG	AAGGAGACCC	GGAAGCTCAA	AGGAGAGTAT	120
CACAAAATTG	CAAGTATAAT	GCAGAAAGTA	GGTAACTYYY	NTTAGATAMN	ATCTTGATTT	180
TNCAGGGTCA	CTGTTATAAG	CTAACAGTAT	AGNAATGTTT	TTATCGTCTT	TCTNKGGNCA	240
TAGACTCCTN	KGAGAAATCTC	TTGAGAACTA	TGATAATGCC	CAGTAAATAC	NCAGATAAGT	300
ATTTAAGGAG	TNCAGATACT	CAAANCCAA	CAATACNGTC	AAAGCATCCT	AGGTTAAGAC	360
AMCNCCCATT	AAATACAGAA	TACCAGCATG	GAAAGGTTCA	GGCTGAGGTT	ATGATTGGGT	420
TTGGGTTTTG	GGNNNGTTT	TTATAAGTCA	TGATTTAAA	AAGAAAAAAT	AAACTCTCTC	480
CAAACATGTA	AAAGTAAGAA	TCTCCTAAA				509

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CAGGAGTGGA	CTAGGTAAAT	GNAAGNTGTT	TTAAAGAGAG	ATGNGNCNG	GGACATAGTG	60
GTACACANCT	GTAATGCTCA	NCACTKATGG	GGAGTACTGA	AGGNGNSGG	ATCACTTGNG	120
GGTCNGGAAT	NTGAGANCAG	CCTGGCAAN	ATGGCGAAC	CCTGTCTCTA	CTAAAAATAG	180
CCANAAWNWA	GCCTAGCGTG	GTGGCGRC	CGCGTGGTTC	CACCTACTCA	GGAGGCNTAA	240
GCACGAGNAN	TNCTTGAACC	CAGGAGGCAG	AGGNTGTGGT	GARCTGAGAT	CGTGCCACTG	300
CACTCCAGTC	TGGCGACMA	AGTGAGACCC	TGTCTCCNNN	AAGAAAAAAA	AAATCTGTAC	360
TTTTTAAGGG	TTGTGGGACC	TGTTAATTAT	ATTGAAATGC	TTCTYTTCTA	GGTCATCCAT	420
GCCTGGCTTA	TTATATCATC	TCTATTGTTG	CTGCTCTTT	TTACATTCCAT	TTACTTGGGG	480

TAAGTTGTGA AATTTGGGGT CTGTCTTCA GAATTAACCA CCTNNGTGCT GTGTAGCTAT	540
CATTTAAAGC CATGTACTTT GNTGATGAAT TACTCTGAAG TTTTAATTGT NTCCACATAT	600
AGGTCACTA TGGTATATAA AAGACTAGNC AGTATTACTA ATTGAGACAT TCTTCTGTNG	660
CTCCTNGCTT ATAATAAGTA GAACTGAAAG NAACCTAAGA CTACAGTTAA TTCTAAGCCT	720
TTGGGGAAAGG ATTATATAGC CTTCTAGTAG GAAAGTCTTGT GCNATCAGAA TGTTNTAAA	780
GAAAGGGTNT CAAGGAATNG TATAAANACC AAAAATAATT GAT	823

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 945 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GTTNTCCNAA CCAACTTAGG AGNTTGGACC TGGGRAAGAC CNACNTGATC TCCGGGAGGN	60
AAAGACTNCA GTTGAGCCGT GATTGCACCC ACTTTACTCC AAGCCTGGC AACCAAAATG	120
AGACACTGGC TCCAAACACA AAAACAAAAA CAAAAAAAGA GTAAATTAAT TTANAGGGAA	180
GNATTAAATA AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGANA	240
TTAATATCTA ATGTTTGGGA GCCATCACAT TATTCTAAAT AATGTTTGG TGGAAATTAT	300
TGTACATCTT TTAAAATCTG TGTAATTTTT TTTCAGGGAA GTGTTAAAA CCTATAACGT	360
TGCTGTGGAC TACATTACTG TTNCACTCCT GATCTGGAAT TTTGGTGTGG TGGGAATGAT	420
TTCCATTCACT TGGAAAGGTC CACTTCGACT CCAGCAGGCA TATCTCATTA TGATTAGTGC	480
CCTCATGNCC CTGKTGTTA TCAAGTACCT CCCTGAATGG ACTGNGTGGC TCATCTTGGC	540
TGTGATTTCA GTATATGGTA AAACCCAAGA CTGATAATTG GTTTGTCACA GGAATGCC	600
ACTGGAGTGT TTTCTTCCT CATCTCTTA TCTTGATTAA GAGAAAATGG TAACGTGTAC	660
ATCCCATAAC TCTTCAGTAA ATCATTAATT AGCTATAGTA ACTTTTCAT TTGAAGATT	720
CGGCTGGCA TGGTAGCTCA TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCAGGCAG	780
ATCACCTAAG CCCAGAGTTC AAGACCAAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA	840
GAAAATACAA AAATTAGCCG GGCATGGTGG TGCACACCTG TAGTTCCAGC TACTTAGGAG	900
GCTGAGGTGG GAGGATCGAT TGATCCCAGG AGGTCAAGNC TGCAG	945

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Tyr Thr Pro Phe
1

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ser Thr Pro Glu
1

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTCACTGA GGACACACC

19

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TGTAGAGCAC CACCAAGA

18

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GCATGGTGTG CATCCACT

18

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GGACCACTCT GGGAGGTA

18

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

AAACTTGGAT TGGGAGAT

18

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Arg Ser Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Lys Asp Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Ser His Leu Gly Pro His Arg Ser Thr Pro Glu Ser Arg Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CAGAGGATGG AGAGAATAC

19

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCTCCCCAA AACTGTCAT

19

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GCCCTAGTGT TCATCAAGTA

20

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AAAGCGGGAG CCAAAGTC

18

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TCACAGAAGA TACCGAGACT

20

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

CCCAACCATA AGAAGAACAG

20

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

TCTGTACTTT TTAAGGGTTG TG

22

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

ACTTCAGAGT AATTCCATCAN CA

22

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GACTCCAGCA GGCATATCT

19

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GATGAGACAA GTNCCNTGAA

20

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TTAGTGGCTG TTTNGTGTCC

20

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CACCCATTAA CAAGTTTAGC

20